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APPLICATION

for

UNITED STATES LETTERS PATENT

on

STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE

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Sheets of Drawings: None
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STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE

[0001] This application claims the benefit under 35 U.S.C. 119(e) of U.S. Serial No. 60/227,866, filed August 24, 2000; U.S. Serial No. 60/264,647, filed January 26, 2001; and U.S. Serial No. 60/300,111, filed June 22, 2001, each of which is incorporated herein by reference in its entirety.

[0002] Three CD-R compact discs, labeled "Copy 1", "Copy 2", and "CRF" and having the files listed below, are submitted herewith and are incorporated herein by reference. Copy 1 and Copy 2 each contain two text documents: 1) a file named SCRIP1300-3_SEQUENCE_LISTING, which contains the Sequence Listing, was created on August 20, 2001 (and recorded on the CD-R on August 21, 2001), and is 9,972 KB in size; and 2) a file named SCRIP1300-3_Table_32, which contains Table 32, was created on August 20, 2001 (and recorded on the CD-R on August 21, 2001), and is 1,251 KB in size. The CRF contains a single file named SCRIP1300-3_SEQUENCE_LISTING, which contains the Sequence Listing, was created on August 20, 2001 (and recorded on the CD-R on August 21, 2001), is 9,972 KB in size, and is identical to the files having the same name on Copy 1 and Copy 2.

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

[0003] The present invention relates generally to plant genes, the expression of which are regulated in response to stress, and more specifically to the gene regulatory elements involved in a stress-induced response in plants, to uses of the coding sequences and regulatory elements of such plant stress-regulated genes, and to transgenic plants genetically modified to express such a coding sequence or to express a heterologous polynucleotide from such a regulatory element.

BACKGROUND INFORMATION

[0004] Microarray technology is a powerful tool that can be used to identify the presence and level of expression of a large number of polynucleotides in a single assay. A microarray is formed by linking a large number of discrete polynucleotide sequences, for example, a population of polynucleotides representative of a genome of an organism, to a solid support such as a microchip, glass slide, or the like, in a defined pattern. By contacting the microarray with a nucleic acid sample obtained from a cell of interest, and detecting those polynucleotides expressed in the cell can hybridize specifically to complementary sequences on the chip, the pattern formed by the hybridizing polynucleotides allows the identification of clusters of genes that are expressed in the cell. Furthermore, where each polynucleotide linked to the solid support is known, the identity of the hybridizing sequences from the nucleic acid sample can be identified.

[0005] A strength of microarray technology is that it allows the identification of differential gene expression simply by comparing patterns of hybridization. For example, by comparing the hybridization pattern of nucleic acid molecules obtained from cells of an individual suffering from a disease with the nucleic acids obtained from the corresponding cells of a healthy individual, genes that are differentially expressed can be identified. The identification of such differentially expressed genes provides a means to identify new genes, and can provide insight as to the etiology of a disease.

[0006] Microarray technology has been widely used to identify patterns of gene expression associated with particular stages of development or of disease conditions in animal model systems, and is being applied to the identification of specific patterns of gene expression in humans. The recent availability of information for the genomes of plants provides a means to adapt microarray technology to the study of plant gene expression.

[0007] Plants and plant products provide the primary sustenance, either directly or indirectly, for all animal life, including humans. For the majority of the world's human population and for many animals, plants and plant products provide the sole source of nutrition. As the world population increases, the best hope to prevent widespread famine is to increase the quantity and improve the quality of food crops, and to make the crops available to the regions of the world most in need of food.

[0008] Throughout history, a continual effort has been made to increase the yield and nutritious value of food crops. For centuries, plants having desirable characteristics such as greater resistance to drought conditions or increased size of fruit were crossbred and progeny plants exhibiting the desired characteristics were selected and used to produce seed or cuttings for propagation. Using such classical genetic methods, plants having, for example, greater disease resistance, increased yield, and better flavor have been obtained. The identification of plant genes involved in conferring a selective advantage on the plant to an environmental challenge would facilitate the generation and yield of plants, thereby increasing the available food supply to an increasing world population. The involvement of these genes in a single organism to responses to multiple stress conditions, however, remains unknown. Thus, a need exists to identify plant genes and polynucleotides that are involved in modulating the response of a plant to changing environmental conditions. The present invention satisfies this need and provides additional advantages.

SUMMARY OF THE INVENTION

[0009] The present invention relates to clusters of genes that are regulated in response to a stress condition in plants. Such clusters include, for example, plant polynucleotides whose expression is altered in response to two or more different stress conditions; and plant polynucleotides the expression of which are altered in response to one stress condition, but not to others. The identification of such clusters, using microarray technology, has allowed the identification of plant stress-regulated genes in *Arabidopsis thaliana* (see Tables 1 and 2); and homologs and orthologs thereof in other plant species (see Table 32). Thus, the invention provides isolated

polynucleotide portions of *Arabidopsis* plant stress-regulated genes, and homologs and orthologs thereof; variants of such sequences, and polynucleotides encoding substantially similar plant stress-regulated polypeptides expressed therefrom. Such sequences include, for example, sequences encoding transcription factors; enzymes, including kinases; and structural proteins, including channel proteins (see Tables 29-31). Accordingly, the present invention also relates to an isolated polynucleotide comprising all or a portion of a plant stress-regulated gene, and to polynucleotide portions thereof, including a coding region (open reading frame), which encodes all or a portion of a stress-regulated polypeptide, for example, as set forth in SEQ ID NOS:1-2703; and a regulatory element involved in regulating the response of the plant to a stress condition such exposure to an abnormal level of salt, osmotic pressure, temperature or any combination thereof, for example, as set forth in SEQ ID NOS:2704-5379.

[0010] The present invention also relates to a recombinant polynucleotide, which contains a nucleotide sequence of a plant stress-regulated gene or functional portion thereof operatively linked to a heterologous nucleotide sequence. In one embodiment, the recombinant polynucleotide comprises a plant stress-regulated gene regulatory element operatively linked to a heterologous nucleotide sequence, which is not regulated by the regulatory element in a naturally occurring plant. The heterologous nucleotide sequence, when expressed from the regulatory element, can confer a desirable phenotype to a plant cell containing the recombinant polynucleotide. In another embodiment, the recombinant polynucleotide comprises a coding region, or portion thereof, of a plant stress-regulated gene operatively linked to a heterologous promoter. The heterologous promoter provides a means to express an encoded stress-regulated polypeptide constitutively, or in a tissue-specific or phase-specific manner.

[0011] Accordingly, in one aspect, the present invention provides an isolated polynucleotide comprising a nucleotide sequence of a plant gene that hybridizes under stringent conditions, preferably high stringency conditions, to any one of SEQ ID NOS:1-5379 (see Tables 1 and 2), including to a coding region (SEQ ID

NOS:1-2703) or a regulatory region, which can alter transcription of an operatively linked nucleic acid sequence in response to an abiotic stress (SEQ ID NOS:2704-5379; see Table 2), or to a complement thereof. Additional aspects provide sequences that hybridize under stringent conditions, preferably high stringency conditions, to the complements of SEQ ID NO 1-1261 (cold responsive genes; Tables 3-6), SEQ ID NOS:2227-2427 (saline responsive genes; Tables 7-10), SEQ ID NOS:2428-2585 (osmotic responsive genes; Tables 11-14), SEQ ID NOS:1699-1969 (cold and osmotic responsive genes; Tables 15-17), SEQ ID NOS:1970-2226 (cold and saline responsive genes; Tables 18-20), SEQ ID NOS:2586-2703 (osmotic and saline responsive genes; Tables 21-23), and SEQ ID NOS:1262-1698(cold, osmotic and saline responsive genes; Tables 24-26), and which can comprise regulatory regions that can alter transcription in response to cold stress, osmotic stress, saline stress, or combinations thereof (SEQ ID NOS:2704-5379; see Table 2). Also provided are nucleotide sequences complementary thereto, and expression cassettes, plants and seeds comprising any of the above isolated sequences.

[0012] In another aspect, the present invention provides an isolated polynucleotide comprising a plant nucleotide sequence that hybridizes under stringent conditions, preferably high stringency conditions, to the complement of any one of SEQ ID NOS:1-2703 (Table 1), including to a coding region thereof (SEQ ID NOS:2704-5379), wherein expression of said coding region is altered in response to an abiotic stress. Additional aspects provide sequences that hybridize under high stringency conditions to the complements of SEQ ID NO 1-1261 (cold responsive genes; Tables 3-6), SEQ ID NOS:2227-2427 (saline responsive genes; Tables 7-10), SEQ ID NOS:2428-2585 (osmotic responsive genes; Tables 11-14), SEQ ID NOS:1699-1969 (cold and osmotic responsive genes; Tables 15-17), SEQ ID NOS:1970-2226 (cold and saline responsive genes; Tables 18-20), SEQ ID NOS:2586-2703 (osmotic and saline responsive genes; Tables 21-23), and SEQ ID NOS:1262-1698(cold, osmotic and saline responsive genes; Tables 24-26), and which can comprise a coding region whose transcription is altered in response to cold stress, osmotic stress, saline stress, or a combination thereof. Also provided are nucleotide

sequences complementary thereto, and expression cassettes, plants and seeds comprising any of the above sequences.

[0013] The invention further relates to a method of producing a transgenic plant, which comprises at least one plant cell that exhibits altered responsiveness to a stress condition. In one embodiment, the method can be performed by introducing a polynucleotide portion of plant stress-regulated gene into a plant cell genome, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cell to a stress condition.

[0014] The polynucleotide portion of the plant stress-regulated gene can encode a stress-regulated polypeptide or functional peptide portion thereof (see SEQ ID NOS:1-2703), wherein expression of the stress-regulated polypeptide or functional peptide portion thereof either increases the stress tolerance of the transgenic plant, or decreases the stress tolerance of the transgenic plant. The polynucleotide portion of the plant stress-regulated gene encoding the stress-regulated polypeptide or functional peptide portion thereof can be operatively linked to a heterologous promoter. The polynucleotide portion of the plant stress-regulated gene also can comprise a stress-regulated gene regulatory element (see SEQ ID NOS:2704-5379). The stress-regulated gene regulatory element can integrate into the plant cell genome in a site-specific manner, whereupon it can be operatively linked to a heterologous nucleotide sequence, which can be expressed in response to a stress condition specific for the regulatory element; or can be a mutant regulatory element, which is not responsive to the stress condition, whereby upon integrating into the plant cell genome, the mutant regulatory element disrupts an endogenous stress-regulated regulatory element of a plant stress-regulated gene, thereby altering the responsiveness of the plant stress-regulated gene to the stress condition.

[0015] In one aspect, the invention provides a method for producing a transgenic plant by introducing into at least one plant cell a recombinant nucleic acid construct comprising i) all or a portion of any one of SEQ ID NOS:1-5379; ii) a polynucleotide

comprising a coding region that hybridizes under conditions of high stringency to all or a portion of the complement of any one of SEQ ID NOS:1-2703; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to abiotic stress, and that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2704-5379; iv) a polynucleotide having at least 90% sequence identity with any one of SEQ ID NO:1-5379; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a nucleotide sequence that alters transcription of an operatively linked coding region in response to abiotic stress; and regenerating a plant from the at least one plant cell.

[0016] Another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1-1261 or 2704-3955; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1-1261; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to cold stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2704-3955; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1-1261 or 2704-3955; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv) wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to cold stress; and regenerating a plant from the at least one plant cell.

[0017] In another aspect, the invention provides a method for producing a transgenic plant by introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2428-2585 or 5108-5263; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high

stringency to the complement of any one of SEQ ID NOS:2428-2585; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to osmotic stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:5108-5263; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:2428-2585 or 5108-5263; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to osmotic stress; and regenerating a plant from the at least one plant cell.

[0018] Still another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2227-2427 or 4910-5107; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2227-2427; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:2227-2427; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:4910-5107; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv) wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to saline stress; and regenerating a plant from the at least one plant cell.

[0019] Yet another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1699-1969 or 4389-4654; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1699-1969; iii) a

polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of cold and osmotic stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:4389-4654; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1699-1969 or 4389-4654; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of cold and osmotic stress; and regenerating a plant from the at least one plant cell.

[0020] Yet another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1970-2226 or 4655-4909; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1970-2226; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of cold and saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:4655-4909; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1970-2226 or 4655-4909; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of cold and saline stress; and regenerating a plant from the at least one plant cell.

[0021] A further aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:2586-2703 or 5264-5379; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high

stringency to the complement of any one of SEQ ID NOS:2586-2703; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of osmotic and saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS: 5264-5379; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:2586-2703 or 5264-5379; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv), wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of osmotic and saline stress; and regenerating a plant from the at least one plant cell.

[0022] Another aspect provides a method for producing a transgenic plant comprising introducing into at least one plant cell a recombinant nucleic acid construct comprising i) any one of SEQ ID NOS:1262-1698 or 3956-4388; ii) a polynucleotide comprising a coding region that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:1262-1698; iii) a polynucleotide comprising a sequence that alters transcription of an operatively linked coding region in response to a combination of cold, osmotic and saline stress that hybridizes under conditions of high stringency to the complement of any one of SEQ ID NOS:3956-4388; iv) a polynucleotide that has at least 90% sequence identity with any one of SEQ ID NOS:1262-1698 or 3956-4388; v) a fragment of any one of the sequences of iv), wherein the fragment comprises a coding region; or vi) a fragment of any one of the sequences of iv) wherein the fragment comprises a sequence or region that alters transcription of an operatively linked coding region in response to a combination of cold, osmotic and saline stress; and regenerating a plant from the at least one plant cell. Further aspects include plants and uniform populations of plants made by the above methods as well as seeds and progeny from such plants.

[0023] In another embodiment, a transgene introduced into a plant cell according to a method of the invention can encode a polypeptide that regulates expression from

an endogenous plant stress-regulated gene. Such a polypeptide can be, for example, a recombinantly produced polypeptide comprising a zinc finger domain, which is specific for the regulatory element, and an effector domain, which can be a repressor domain or an activator domain. The polynucleotide encoding the recombinant polypeptide can be operatively linked to and expressed from a constitutively active, inducible or tissue specific or phase specific regulatory element. Expression of the recombinant polypeptide from a plant stress-regulated promoter as disclosed herein can be particularly advantageous in that the polypeptide can be coordinately expressed with the endogenous plant stress-regulated genes upon exposure to a stress condition. The invention also provides transgenic plants produced by a method as disclosed, as well as to a plant cell obtained from such transgenic plant, wherein said plant cell exhibits altered responsiveness to the stress condition; a seed produced by the transgenic plant; and a cDNA or genomic DNA library prepared from the transgenic plant, or from a plant cell from said transgenic plant, wherein said plant cell exhibits altered responsiveness to the stress condition.

[0024] In one aspect, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence substantially similar to a sequence of any one of SEQ ID NOS:2704-5379, which can alter transcription of an operatively linked polynucleotide in a plant cell in response to an abiotic stress. Additional aspects of the invention provide isolated polynucleotides, including, for example, sequences substantially similar to any of SEQ ID NOS:2704-3955, which can alter transcription of an operatively linked polynucleotide in response to a cold stress; isolated polynucleotides substantially similar to a sequence of any of SEQ ID NOS:5108-5263, which can alter transcription of an operatively linked polynucleotide in response to an osmotic stress; isolated polynucleotides substantially similar to a sequence of any of SEQ ID NOS:4910-5107, which can alter transcription of an operatively linked polynucleotide in response to a saline stress; isolated polynucleotides substantially similar to a sequence of any of SEQ ID NOS:4389-4654, which can alter transcription of an operatively linked polynucleotide in response to a combination of cold and osmotic stresses; isolated polynucleotides

substantially similar to a sequence of any of SEQ ID NOS:4655-4909, which can alter transcription of an operatively linked polynucleotide in response to a combination of cold and saline stresses; isolated polynucleotides substantially similar to a sequence of any of SEQ ID NOS:5264-5379, which can alter transcription of an operatively linked polynucleotide in response to a combination of osmotic and saline stresses; and isolated polynucleotides substantially similar to a sequence of any of SEQ ID NOS:3956-4388, which can alter transcription of an operatively linked polynucleotide in response to a combination of cold, osmotic and saline stresses.

[0025] Related aspects of the invention provide an isolated nucleotide sequences that can alter transcription of an operatively linked polynucleotide in response to an abiotic stress, and that hybridize under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:2704-5379. Additional aspects provide an isolated nucleotide sequence that can alter transcription of an operatively linked polynucleotide in response to cold stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:2704-3955; a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response to osmotic stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:5108-5263; a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response to saline stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:4910-5107; a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response to a combination of cold and osmotic stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:4389-4654; a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response to a combination of cold and saline stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:4655-4909; a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response

to an combination of osmotic and saline stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:5264-5379; and a nucleotide sequence that alters transcription of an operatively linked polynucleotide in response to a combination of cold, osmotic and saline stress, and that hybridizes under stringent conditions, preferably highly stringent conditions, to the complement of any one of SEQ ID NOS:3956-4388.

[0026] Further aspects provide an expression cassette comprising as operatively linked components any of the above isolated nucleic acid sequences that alter transcription, a coding region, and a termination sequence. Also provided are host cells and seeds comprising such expression cassettes, plants containing such host cells and seeds and progeny of plants containing said host cells. In related aspects, the coding region of the expression cassettes comprise sequences encoding marker proteins and sequences involved in gene silencing such as antisense sequences, double stranded RNAi sequences, a triplexing agent, and sequences comprising dominant negative mutations. In additional related aspects, the coding regions comprise sequences encoding polypeptides that alter the response of a plant to an abiotic stress.

[0027] The present invention also relates to a method of modulating the responsiveness of a plant cell to a stress condition. Such a method can be performed, for example, by introducing a polynucleotide portion of a plant stress-regulated genes described herein into the plant cell, thereby modulating the responsiveness of the plant cell to a stress condition. Such a method can result in the responsiveness of the plant cell being increased upon exposure to the stress condition, which, in turn, can result in increased or decreased tolerance of the plant cell to a stress condition; or can result in the responsiveness of the plant cell to the stress condition being decreased, which, in turn, can result in increased or decreased tolerance of the plant cell to a stress condition. In one embodiment, the polynucleotide portion of the plant stress-regulated gene can integrate into the genome of the plant cell, thereby modulating the responsiveness of the plant cell to the stress condition. In another embodiment, the polynucleotide portion of the plant stress-regulated gene encodes a stress-regulated

polypeptide or functional peptide portion thereof, and can be operatively linked to a heterologous promoter. The polynucleotide portion of the plant stress-regulated gene also can contain a mutation, whereby upon integrating into the plant cell genome, the polynucleotide disrupts (knocks-out) an endogenous plant stress-regulated sequence, thereby modulating the responsiveness of the plant cell to the stress condition. Depending on whether the knocked-out gene encodes an adaptive or a maladaptive stress-regulated polypeptide, the responsiveness of the plant will be modulated accordingly.

[0028] The present invention further relates to a method of modulating the activity of a biological pathway in a plant cell, wherein the pathway involves a stress-regulated polypeptide or a non-protein regulatory molecule. Such a method can be performed by introducing a polynucleotide portion of a plant stress-regulated gene, or a polynucleotide derived therefrom, for example a ribozyme derived from a nucleotide sequence as set forth in any of SEQ ID NOS:1-2703, into the plant cell, thereby modulating the activity of the biological pathway. The method can be performed with respect to a pathway involving any of the stress-regulated polypeptides as disclosed herein or encoded by the polynucleotides disclosed herein, as well as using homologs or orthologs thereof. In one embodiment, the method is performed by introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, wherein the plant stress-regulated gene comprises a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, thereby modulating the activity of the biological pathway.

[0029] The present invention also relates to a method of identifying a polynucleotide that modulates a stress response in a plant cell. In one embodiment the method comprises determining gene expression in a plant exposed to at least one stress to produce an expression profile and identifying sequences whose expression is altered at least two fold compared to plants not exposed to the stress. Such an expression profile can be obtained, for example, by contacting an array of probes representative of a plant cell genome with nucleic acid molecules expressed in a plant cell exposed to the stress; and detecting one or more nucleic acid molecules expressed at a level different from a level of expression in the absence of the stress. The method can further comprise introducing the differentially expressed nucleic acid molecule into a plant cell; and detecting a modulated response of the genetically modified plant cell to a stress, thereby identifying a polynucleotide that modulates a stress response in a plant cell. The stress can be any stress, for example, an abiotic stress such as exposure to an abnormal level of cold, osmotic pressure, and salinity. The contacting is under conditions that allow for selective hybridization of a nucleic acid molecule with probe having sufficient complementarity, for example, under stringent hybridization conditions. Expression of the nucleic acid molecule can increase or decrease the tolerance of the plant cell to the stress, and the nucleic acid molecule can be expressed at a level that is less than or greater than the level of expression in the absence of the stress.

[0030] In still another embodiment, the polynucleotide portion of the plant stress-regulated gene can comprise a stress-regulated regulatory element, which can be operatively linked to a heterologous nucleotide sequence, the expression of which can modulate the responsiveness of the plant cell to a stress condition. Such a heterologous nucleotide sequence can encode, for example, a stress-inducible transcription factor such as DREB1A. The heterologous nucleotide sequence also can encode a polynucleotide that is specific for a plant stress-regulated gene, for example, an antisense molecule, an RNAi molecule, a ribozyme, and a triplexing agent, any of which, upon expression in the plant cell, reduces or inhibits expression of a stress-regulated polypeptide encoded by the gene, thereby modulating the responsiveness of

the plant cell to a stress condition, for example, an abnormal level of cold, osmotic pressure, and salinity. In another aspect, the method can include introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, wherein the plant stress-regulated gene includes a nucleotide sequence of a polynucleotide as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1725, 1727-1865, 1867-1917, 1919-1927, 1929-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, thereby modulating the responsiveness of the plant cell to a stress condition. The invention also relates to a plant cell obtained by any of the methods of modulating the responsiveness of a plant to a stress condition or combination of stress conditions, and to a plant comprising such a plant cell.

[0031] The present invention further relates to a method of selecting a plant having an altered resistance to an abiotic stress condition or a combination of abiotic stress conditions, such a method being useful for marker-assisted breeding. Such a method can be performed, for example, by contacting nucleic acid molecules representative of expressed polynucleotides in a plant cell of a plant to be examined for having an altered resistance to an abiotic stress with a nucleic acid probes that selectively hybridizes under stringent conditions to a plant stress-regulated gene comprising a nucleotide sequence as set forth in any of SEQ ID NO:1-5379; detecting a level of selective hybridization of the nucleic acid probes to a nucleic acid molecule representative of an expressed polynucleotide in the plant cell, wherein the level of selective hybridization corresponds to the level of the expressed polynucleotide in the plant cell, which is indicative of resistance of the plant to an abiotic stress; and selecting a plant having a level of expression of a polynucleotide indicative of altered resistance to an abiotic stress condition. For example, the abiotic stress condition can be cold stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-1261 and 2704-3955, for

example, at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261, 2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, and 3313-3955; or the abiotic stress condition can be saline stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 and 4910-5107; or the abiotic stress condition can be osmotic stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2428-2585 and 5108-5263. In addition, a combination of abiotic stress conditions can be a combination of cold stress and osmotic stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1669-1969 and 4389-4654, for example, at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1725, 1727-1865, 1867-1917, 1919-1927, 1929-1969, 4389-4414, 4416-4552, 4554-4602, 4604-4612, and 4613-4654; or the combination of abiotic stress conditions can be a combination of cold stress and saline stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1970-2226 and 4655-4909; or the combination of abiotic stress conditions can be a combination of osmotic stress and saline stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703 and 5264-5379; or the combination of abiotic stress conditions can be a combination of cold stress, osmotic stress and saline stress, and the nucleic acid probe can include at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698 and 3956-4388, for example, at least about 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262, 1264-1386, 1387-1390, 1392-1404, 1406-1444, 1446-1483, 1485-1588, 1590-1608, 1610-1633, 1634-1698, 3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, and 4326-4388.

[0032] The present invention also relates to a method of expressing a heterologous nucleotide sequence in a plant cell. Such a method can be performed, for example, by introducing into the plant cell a plant stress-regulated regulatory element operatively linked to the heterologous nucleotide sequence, whereby, upon exposure of the plant cell to a stress condition, the heterologous nucleotide sequence is expressed in the plant cell. In one embodiment, the stress-regulated gene regulatory element is any of the sequences described herein that are capable of altering transcription of an operatively linked sequence in response to an abiotic stress, for example, SEQ ID NOS:2704-5379. In another embodiment, stress-regulated gene regulatory element comprises a nucleotide sequence as set forth in any of SEQ ID NOS:2704-2855, 2857-2928, 2930-2932, 2934-3256, 3258-3271, 3273-3304, 3306-3323, 3325-3333, 3335-3485, 3487-3511, 3313-3956, 3958-4078, 4080-4097, 4099-4136, 4138-4175, 4177-4279, 4281-4299, 4301-4324, 4326-4414, 4416-4552, 4554-4602, and 4604-5379, whereby, upon exposure of the plant cell to stress condition, the heterologous nucleotide sequence is expressed in the plant cell. The heterologous nucleotide sequence can encode a selectable marker, a diagnostic marker, or a polypeptide that confers a desirable trait upon the plant cell, for example, a polypeptide that improves the nutritional value, digestibility or ornamental value of the plant cell, or a plant comprising the plant cell.

[0033] The present invention additionally relates to a method of identifying a stress condition to which a plant cell was exposed by comparing an expression profile from a test plant suspected of having been exposed to at least one stress condition to an expression profile obtained from a reference plant, preferably of the same species, which has been exposed to the suspected stress condition. Such a method can be performed, for example, by contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence, wherein the probe comprises at least 15 nucleotides of a plant stress-regulated gene, wherein the stress-regulated gene does not have a nucleotide sequence of a polynucleotide as set forth in any of SEQ ID NOS:156, 229, 233, 558, 573, 606,

635, 787, 813, 1263, 1386, 1391, 1405, 1445, 1484, 1589, 1609, 1634, 1726, 1866, 1918 or 1928,or a nucleotide sequence complementary thereto, whereby detecting selective hybridization of at least one nucleic acid probe, or detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to an abiotic stress, indicates that the test plant has been exposed to an abiotic stress, and whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to an abiotic stress. For example, the abiotic stress is cold stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1-155, 157-228, 230-232, 234-557, 559-572, 574-605, 607-634, 636-786, 788-812, 814-1261 or a nucleotide sequence complementary thereto; or the abiotic stress can be a saline stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2226-2427 or a nucleotide sequence complementary thereto; or the abiotic stress can be an osmotic stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in two or more of SEQ ID NOS:2428-2585 or a nucleotide sequence complementary thereto.

[0034] A method of identifying a stress condition to which a plant cell was exposed also can be performed, for example, by contacting nucleic acid molecules expressed in the test plant cell with an array of probes representative of the plant cell genome; detecting a profile of expressed nucleic acid molecules characteristic of a stress response, and comparing the expression pattern in the test plant to the expression pattern obtained from a reference plant thereby identifying the stress condition to which the plant cell was exposed. The contacting is under conditions that allow for selective hybridization of a nucleic acid molecule with probes having sufficient complementarity, for example, under stringent hybridization conditions. The profile can be characteristic of exposure to a single stress condition, for example, an abnormal level of cold, osmotic pressure, or salinity, or can be characteristic of exposure to more than one stress condition, for example, cold, increased osmotic

pressure and increased salinity. In one embodiment, the nucleotide sequence of a gene whose expression is detected is selected from a polynucleotide comprising any of SEQ ID NOS:1-2703. In further embodiments, the nucleotide sequence of a gene that is expressed in response a particular stress or combination of stresses can comprise a polynucleotide expressed in response to cold stress (SEQ ID NOS:1-1261), osmotic stress (SEQ ID NOS:2428-2585), saline (salt) stress (SEQ ID NOS:2227-2427), a combination of cold and osmotic stress (SEQ ID NOS:1699-1969), a combination of saline and osmotic stress (SEQ ID NOS:1970-2226), a combination of osmotic and saline stress (SEQ ID NOS:2586-2703), or a combination of cold, osmotic and saline stress (SEQ ID NOS:1262-1698).

[0035] In another embodiment, the method can be used for determining whether a test plant has been exposed to a combination of abiotic stress conditions. Such a method can be performed, for example, by contacting nucleic acid molecules representative of expressed polynucleotides in cells of the test plant with at least one nucleic acid probe under conditions suitable for selective hybridization to a complementary nucleotide sequence, whereby detecting selective hybridization of at least one nucleic acid probe, or detecting a change in a level of selective hybridization as compared to a level of selective hybridization obtained using nucleic acid molecules representative of expressed polynucleotides in cells of a plant known not have been exposed to a combination of stress conditions, indicates that the test plant has been exposed to a combination of abiotic stress conditions, and whereby an absence of selective hybridization of at least one nucleic acid probe indicates that the test plant has not been exposed to a combination of abiotic stress conditions. For example, the combination of abiotic stress conditions can be a combination of a cold stress and an osmotic stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1699-1969, or a nucleotide sequence complementary thereto; or the combination of abiotic stress conditions can be a combination of a cold stress and a saline stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID

NOS:1970-2226, or a nucleotide sequence complementary thereto; or the combination of abiotic stress conditions can be a combination of an osmotic stress and a saline stress, and the probe can included at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:2586-2703, or a nucleotide sequence complementary thereto; or the combination of abiotic stress conditions can be a combination of a cold stress, a saline stress and an osmotic stress, and the probe can include at least 15 nucleotides of a nucleotide sequence as set forth in any of SEQ ID NOS:1262-1698, or a nucleotide sequence complementary thereto.

[0036] The present invention also relates to a method for monitoring a population of plants for exposure to a stress condition or combination of stress conditions. Such a method can be performed, for example, by introducing into the population of a plants a sentinel plant, wherein said sentinel plant is a transgenic plant, which contains plant cells containing a stress-regulated regulatory element operatively linked to a polynucleotide encoding a detectable marker; and examining the sentinel plant for expression of the detectable marker, which is indicative of exposure of the population of plants to a stress condition or combination of stress conditions. The stress condition or combination of stress conditions can be any such condition or conditions, particularly an abiotic stress condition or combination of abiotic stress conditions. The detectable marker can be any reporter molecule that is readily or conveniently detectable, particularly a marker that is visibly detectable, for example, a luminescent detectable marker such as luciferin, or a fluorescent detectable marker such as a green fluorescent protein, a yellow fluorescent protein, a cyan fluorescent protein, a red fluorescent protein, or an enhanced or modified form thereof.

[0037] The present invention further relates to a transgenic plant, which contains a nucleic acid construct comprising a polynucleotide portion of plant stress-regulated polynucleotide. In one embodiment, the transgenic plant exhibits altered responsiveness to a stress condition as compared to a corresponding reference plant not containing the construct. Such a transgenic plant can contain, for example, a construct that disrupts an endogenous stress-regulated gene in the plant, thereby

reducing or inhibiting expression of the gene in response to a stress condition. Such a knock-out can increase or decrease tolerance of the plant to a stress condition. The transgene also can comprise a coding sequence of a plant stress-regulated gene, which can be operatively linked to a heterologous regulatory element such as a constitutively active regulatory element, an regulated regulatory element, a tissues specific or phase specific regulatory element, or the like. In another embodiment, the transgenic plant contains a nucleic acid construct comprising a plant stress-regulated regulatory element, which can be operatively linked to a heterologous nucleotide sequence that can encode a polypeptide. Expression of the heterologous polypeptide can confer a desirable characteristic on the plant, for example, can improve the nutritional or ornamental value of the transgenic plant. In still another embodiment, the transgenic plant contains multiple nucleic acid constructs, which can be multiple copies of the same construct, or can be two or more different constructs.

[0038] The present invention also relates to a plant stress-regulated regulatory element, which is obtained from a plant stress-regulated polynucleotide disclosed herein for example any of SEQ ID NOS:2704-5379; a homolog or ortholog thereof. The invention also provides a method of identifying an agent, for example a transcription factor, that specifically binds to or activates a plant stress-regulated regulatory element. Such a method can be performed, for example, by contacting the regulatory element with a plant cell extract, and identifying polypeptides that specifically bind to the regulatory element. Confirmation that the specifically binding polypeptide is a transcription factor can be demonstrated using, for example, the stress-regulated regulatory element operably linked to a reporter gene, and detecting expression of the reporter gene. Control constructs comprising a regulatory element, other than a plant stress-regulated regulatory element, operatively linked to a reporter molecule can be used to confirm that the transcription factor is specific for the plant stress-regulated regulatory element. A polynucleotide encoding such a transcription factor also can be obtained.

[0039] The present invention also relates to a method of using a polynucleotide portion of a plant stress-regulated gene to confer a selective advantage on a plant cell. In one embodiment, such a method is performed by introducing a plant stress-regulated regulatory element into a plant cell such as those described herein, wherein, upon exposure of the plant cell to a stress condition to which the regulatory element is responsive, a nucleotide sequence operatively linked to the regulatory element is expressed, thereby conferring a selective advantage to plant cell. The operatively linked nucleotide sequence can be, for example, a transcription factor, the expression of which induces the further expression of polynucleotides involved in a stress response, thereby enhancing the response of a plant to the stress condition. In another embodiment, a coding sequence of a plant stress-regulated gene as disclosed herein is introduced into the cell, thereby providing the plant with a selective advantage in response to a stress condition. In still another embodiment, the method results in the knock-out of a plant stress-regulated gene as disclosed herein in a first population of plants, thereby providing a selective advantage to a stress condition in a second population of plants.

[0040] The invention further relates to a method of identifying an agent that modulates the activity of a stress-regulated regulatory element of a plant. In a particular embodiment, is provided a method for identifying an agent that alters the activity of an abiotic stress responsive regulatory element comprising contacting the agent or a composition containing an agent to be tested with at least one abiotic stress responsive regulatory element, preferably selected from the group consisting of SEQ ID NOS:2704-5379 (see Table 2), and determining the effect of the agent on the ability of the regulatory sequence to regulate transcription. In further embodiments, the regulatory elements are associated with particular stresses or combination of stresses such as cold stress (SEQ ID NOS:2704-3955), osmotic stress (SEQ ID NOS:5108-5263), saline stress (SEQ ID NOS:4910-5107), a combination of cold and osmotic stress (SEQ ID NOS:4389-4654), a combination of cold and saline stress (SEQ ID NOS:4655-4909), a combination of osmotic and saline stress (SEQ ID NOS:5264-5379), or a combination of cold, osmotic and saline stress (SEQ ID

NOS:3956-4388). In one embodiment, the regulatory element can be operatively linked to a heterologous polynucleotide encoding a reporter molecule, and an agent that modulates the activity of the stress-regulated regulatory element can be identified by detecting a change in expression of the reporter molecule due to contacting the regulatory element with the agent. Such a method can be performed *in vitro* in a plant cell-free system, or in a plant cell in culture or in a plant *in situ*. In another embodiment, the agent is contacted with a transgenic plant containing an introduced plant stress-regulated regulatory element, and an agent that modulates the activity of the regulatory element is identified by detecting a phenotypic change in the transgenic plant. The methods of the invention can be performed in the presence or absence of the stress condition to which the particularly regulatory element is responsive.

[0041] Another aspect provides a method for identifying an agent that alters abiotic stress responsive polynucleotide expression in a plant or plant cell comprising contacting a plant or plant cell with a test agent; subjecting the plant cell or plant cell to an abiotic stress or combination of stresses before, during or after contact with the agent to be tested; obtaining an expression profile of the plant or plant cell and comparing the expression profile of the plant or plant cell to an expression profile from a plant or plant cell not exposed to the abiotic stress or combination of stresses. In one embodiment, the expression profile comprises expression data for at least one nucleotide sequence comprising any of SEQ ID NOS:1-5379 (see Tables 1 and 2). In additional embodiments, the expression profile comprises expression data for at least one, and preferably two or more sequences associated with a particular abiotic stress or combination of stresses such as cold stress (SEQ ID NOS:1-1261 and 2704-3955), osmotic stress (SEQ ID NOS:2428-2585 and 5108-5263), saline stress (SEQ ID NOS:2227-2427 and 4910-5107), a combination of cold and osmotic stress (SEQ ID NOS:1699-1969 and 4389-4654), a combination of cold and saline stress (SEQ ID NOS:1970-2226 and 4655-4909), a combination of osmotic and saline stress (SEQ ID NOS:2586-2703 and 5264-5379), or a combination of cold, osmotic and saline stress (SEQ ID NOS:1262-1698 and 3956-4388).

[0042] Still another aspect provides nucleotide probes useful for detecting an abiotic stress response in plants, the probes comprising a nucleotide sequence of at least 15, 25, 50 or 100 nucleotides that hybridizes under stringent, preferably highly stringent, conditions to at least one sequence comprising any of SEQ ID NOS:1-2703. Also provided are nucleotide probes comprising at least 15, 25, 50 or 100 nucleotides in length that hybridize under stringent, preferably highly stringent conditions, to at least one gene associated with a particular stress or combination of stresses, for example cold stress, (SEQ ID NOS:1-1261), osmotic stress (SEQ ID NOS:2428-2585), saline stress (SEQ ID NOS:2227-2427), a combination of cold and osmotic stress (SEQ ID NOS:1699-1969), a combination of cold and saline stress (SEQ ID NOS:1970-2226), a combination of osmotic and saline stress (SEQ ID NOS:2586-2703), or a combination of cold, osmotic, and saline stress (SEQ ID NOS:1262-1698).

[0043] An additional aspect provides a method for marker-assisted breeding to select plants having an altered resistance to abiotic stress comprising obtaining nucleic acid molecules from the plants to be selected; contacting the nucleic acid molecules with one or more probes that selectively hybridize under stringent, preferably highly stringent, conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1-2703; detecting the hybridization of the one or more probes to the nucleic acid sequences wherein the presence of the hybridization indicates the presence of a gene associated with altered resistance to abiotic stress; and selecting plants on the basis of the presence or absence of such hybridization. Marker-assisted selection can also be accomplished using one or more probes which selectively hybridize under stringent, preferably highly stringent conditions, to a nucleotide sequence comprising a polynucleotide expressed in response associated with a particular stress, for example, a nucleotide sequence comprising any of SEQ ID NOS:1-1261 (cold stress), SEQ ID NOS:2428-2585 (osmotic stress), SEQ ID NOS:2227-2427 (saline stress), SEQ ID NOS:1699-1969 (cold and osmotic stress), SEQ ID NOS:1970-2226 (cold and saline stress), SEQ ID NOS:2586-2703 (osmotic and saline stress), or SEQ ID NOS:1262-1698 (cold, osmotic and saline stress). In

each case marker-assisted selection can be accomplished using a probe or probes to a single sequence or multiple sequences. If multiple sequences are used they can be used simultaneously or sequentially.

[0044] A further aspect provides a method for monitoring a population of plants comprising providing at least one sentinel plant containing a recombinant polynucleotide comprising a stress responsive regulatory sequence selected from the group consisting of SEQ ID NOS:2704-5379 which is operatively linked to a nucleotide sequence encoding a detectable marker, for example a fluorescent protein. Additional aspects provide the use of various regulatory sequences including those associated with cold stress (SEQ ID NOS:2704-3955), osmotic stress (SEQ ID NOS:5108-5263), saline stress (SEQ ID NOS:4910-5107), cold and osmotic stress (SEQ ID NOS:4389-4654), cold and saline stress (SEQ ID NOS:4655-4909), osmotic and saline stress (SEQ ID NOS:5264-5379), and cold, osmotic and saline stress (SEQ ID NOS:3956-4388), or fragments thereof wherein such fragments can alter transcription of an operatively linked nucleotide sequence in response to an abiotic stress.

[0045] A further aspect provides a computer readable medium having stored thereon computer executable instructions for performing a method comprising receiving data on gene expression in a test plant of at least one nucleic acid molecule having at least 70%, preferably at least 80%, more preferably at least 90%, and most preferably at least 95% nucleotide sequence identity to one or more polynucleotide sequences as set forth in any of SEQ ID NOS:1-2703; and comparing expression data from the test plant to expression data for the same polynucleotide sequence or sequences in a plant that has been exposed to at least one abiotic stress.

[0046] Yet a further aspect provides a computer readable medium having stored thereon a data structure comprising, sequence data for at least one, and preferably a plurality of nucleic acid molecules having at least 70%, preferably at least 80%, more preferably at least 90%, and most preferably at least 95% nucleotide sequence identity

to a polynucleotide comprising any of SEQ ID NOS:1-2703, or the complement thereof; and a module receiving the nucleic acid molecule sequence data which compares the nucleic acid molecule sequence data to at least one other nucleic acid sequence.

DETAILED DESCRIPTION OF THE INVENTION

[0047] The present invention relates to clusters of genes that are induced in response to one or a combination of abiotic stress conditions. Abiotic stress conditions, such as a shortage or excess of solar energy, water and nutrients, and salinity, high and low temperature, or pollution (e.g., heavy metals), can have a major impact on plant growth and can significantly reduce the yield, for example, of cultivars. Under conditions of abiotic stress, the growth of plant cells is inhibited by arresting the cell cycle in late G1, before DNA synthesis, or at the G2/M boundary (see Dudits, Plant Cell Division, Portland Press Research, Monograph; Francis, Dudits, and Inze, eds., 1997; chap. 2, page 21; Bergounioux, Protoplasma 142:127-136, 1988). The identification of stress-regulated gene clusters, using microarray technology, provides a means to identify plant stress-regulated genes.

[0048] As used herein, the term "cluster," when used in reference to stress-regulated genes, refers to nucleotide sequences of genes that have been selected by drawing Venn diagrams, and selecting those genes that are regulated only by a selected stress condition. In general, a cluster of stress-regulated genes includes at least 5, 10, 15, or 20 genes, including polynucleotide portions thereof, each of which is responsive to the same selected stress condition or conditions. The selected stress condition can be a single stress condition, for example, cold, osmotic stress or salinity stress (see Tables 3-14), or can be a selected combination of stress conditions, for example, cold, osmotic stress and salinity stress (see Tables 15-26). In addition, a cluster can be selected based on specifying that all of the genes are coordinately regulated, for example, they all start at a low level and are induced to a higher level. However, a cluster of saline stress-regulated genes, for example, that was selected for coordinate regulation from low to high, also can be decreased in response to cold or

mannitol. By varying the parameters used for selecting a cluster of gene nucleotide sequences, those genes that are expressed in a specific manner following a stress can be identified.

[0049] As used herein in reference to a polynucleotide or polynucleotide portion of a gene or nucleic acid molecule, the term "isolated" means a polynucleotide, polynucleotide portion of a gene, or nucleic acid molecule that is free of one or both of the nucleotide sequences that normally flank the polynucleotide in a genome of a naturally-occurring organism from which the polynucleotide is derived. The term includes, for example, a polynucleotide or fragment thereof that is incorporated into a vector or expression cassette; into an autonomously replicating plasmid or virus; into the genomic DNA of a prokaryote or eukaryote; or that exists as a separate molecule independent of other polynucleotides. It also includes a recombinant polynucleotide that is part of a hybrid polynucleotide, for example, one encoding a polypeptide sequence.

[0050] The terms "polynucleotide," "oligonucleotide," and "nucleic acid sequence" are used interchangeably herein to refer to a polymeric (2 or more monomers) form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. Although nucleotides are usually joined by phosphodiester linkages, the term also includes polymers containing neutral amide backbone linkages composed of aminoethyl glycine units. The terms are used only to refer to the primary structure of the molecule. Thus, the term includes double stranded and single stranded DNA molecules, including a sense strand or an antisense strand, and RNA molecules as well as genomic DNA, cDNA, mRNA and the like. It will be recognized that such polynucleotides can be modified, for example, by including a label such as a radioactive, fluorescent or other tag, by methylation, by the inclusion of a cap structure, by containing a substitution of one or more of the naturally occurring nucleotides with a nucleotide analog, by containing an internucleotide modification such as having uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, or the like), by containing a pendant moiety such as a

protein (e.g., a nuclease, toxin, antibody, signal peptide, poly-L-lysine, or the like), by containing an intercalator such as acridine or psoralen, by containing a chelator, which can be a metal such as boron, an oxidative metal, or a radioactive metal, by containing an alkylator, or by having a modified linkage (e.g., an alpha anomeric nucleic acid).

[0051] The term "recombinant nucleic acid molecule" refers to a polynucleotide produced by human intervention. A recombinant nucleic acid molecule can contain two or more nucleotide sequences that are linked in a manner such that the product is not found in a cell in nature. In particular, the two or more nucleotide sequences can be operatively linked and, for example, can encode a fusion polypeptide, or can comprise a nucleotide sequence and a regulatory element. A recombinant nucleic acid molecule also can be based on, but different, from a naturally occurring polynucleotide, for example, a polynucleotide having one or more nucleotide changes such that a first codon, which normally is found in the polynucleotide, is replaced with a degenerate codon that encodes the same or a conservative amino acid, or such that a sequence of interest is introduced into the polynucleotide, for example, a restriction endonuclease recognition site or a splice site, a promoter, a DNA replication initiation site, or the like.

[0052] As used herein, the term "abiotic stress" or "abiotic stress condition" refers to the exposure of a plant, plant cell, or the like, to a non-living ("abiotic") physical or chemical agent or condition that has an adverse effect on metabolism, growth, development, propagation and/or survival of the plant (collectively "growth"). An abiotic stress can be imposed on a plant due, for example, to an environmental factor such as water (e.g., flooding, drought, dehydration), anaerobic conditions (e.g., a low level of oxygen), abnormal osmotic conditions, salinity or temperature (e.g., hot/heat, cold, freezing, frost), a deficiency of nutrients or exposure to pollutants, or by a hormone, second messenger or other molecule. Anaerobic stress, for example, is due to a reduction in oxygen levels (hypoxia or anoxia) sufficient to produce a stress response. A flooding stress can be due to prolonged or transient immersion of a plant,

plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, or the like. A cold stress or heat stress can occur due to a decrease or increase, respectively, in the temperature from the optimum range of growth temperatures for a particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art. Dehydration stress can be induced by the loss of water, reduced turgor, or reduced water content of a cell, tissue, organ or whole plant. Drought stress can be induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism. Saline stress (salt stress) can be associated with or induced by a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell. Osmotic stress also can be associated with or induced by a change, for example, in the concentration of molecules in the intracellular or extracellular environment of a plant cell, particularly where the molecules cannot be partitioned across the plant cell membrane.

[0053] As disclosed herein, clusters of plant stress-regulated genes (Example 1; see, also, Tables 1-31) and homologs and orthologs thereof (Table 32) have been identified. Remarkably, several of the stress-regulated genes previously were known to encode polypeptides having defined cellular functions, including roles as transcription factors, enzymes such as kinases, and structural proteins such as channel proteins (see Tables 29-31). The identification of *Arabidopsis* stress-regulated genes provides a means to identify homologous and orthologous genes and gene sequences in other plant species using well known procedures and algorithms based on identity (or homology) to the disclosed sequences. Thus, the invention provides polynucleotide sequences comprising plant stress-regulated genes that are homologs or orthologs, variants, or otherwise substantially similar to the polynucleotides disclosed herein, and having an E value $\leq 1 \times 10^{-8}$, which can be identified, for example, by a BLASTN search using the *Arabidopsis* polynucleotides of Tables 1 and 2 (SEQ ID NOS:1-5379) as query sequences (see Table 32, on CD).

[0054] A polynucleotide sequence of a stress-regulated gene as disclosed herein can be particularly useful for performing the methods of the invention on a variety of plants, including but not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea ultilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*).Ornamentals such as azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum are also included. Additional ornamentals within the scope of the invention include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Conifers that may be employed in

practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga ultilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*).

[0055] Leguminous plants which may be used in the practice of the present invention include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mung bean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

[0056] Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, ultilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, ultilane, chicory, groundnut and zucchini.

[0057] As used herein, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence corresponding to a reference nucleotide sequence, wherein the corresponding sequence encodes a polypeptide or comprises a regulatory element having substantially the same structure and function as the polypeptide encoded by the reference nucleotide sequence, for example, where only changes in amino acids not affecting the polypeptide function occur. For purposes of the present invention, a reference (or query) sequence is a polynucleotide sequence as set forth in any of SEQ ID NOS:1-2703 or a polypeptide encoded thereby. Desirably, a substantially similar nucleotide sequence encodes the polypeptide encoded by the reference nucleotide sequence. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence desirably is at least 60%, more desirably at least 75%, preferably at least 90%, more preferably at least 95%, still more preferably at least 99% and including 100%. A nucleotide sequence is "substantially similar" to reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C (stringent conditions), more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C (high stringency), preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C (very high stringency), more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C (extremely high stringency).

[0058] In addition, the term "substantially similar," when used in reference to a polypeptide sequence, means that an amino acid sequence relative to a reference (query) sequence shares at least about 65% amino acid sequence identity, particularly at least about 75% amino acid sequence identity, and preferably at least about 85%,

more preferably at least about 90% , and most preferably at least about 95% or greater amino acid sequence identity. Generally, sequences having an $E \leq 10^{-8}$ are considered to be substantially similar to a query sequence. Such sequence identity can take into account conservative amino acid changes that do not substantially affect the function of a polypeptide. As such, homologs or orthologs of the *Arabidopsis* stress-regulated nucleotide sequences disclosed herein, variants thereof, and polypeptides substantially similar to the polynucleotide sequence of *Arabidopsis* stress-regulated genes set forth in SEQ ID NOS:1-5379 are encompassed within the present invention and, therefore, useful for practicing the methods of the invention (see, for example, Table 32, which is on the CD-R filed herewith, and incorporated herein by reference).

[0059] Homology or identity is often measured using sequence analysis software such as the Sequence Analysis Software Package of the Genetics Computer Group (University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. The terms "homology" and "identity," when used herein in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or of nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection.

[0060] For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0061] The term "comparison window" is used broadly herein to include reference to a segment of any one of the number of contiguous positions, for example, about 20 to 600 positions, for example, amino acid or nucleotide position, usually about 50 to about 200 positions, more usually about 100 to about 150 positions, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, for example, by the local homology algorithm of Smith and Waterman (Adv. Appl. Math. 2:482, 1981), by the homology alignment algorithm of Needleman and Wunsch (J. Mol. Biol. 48:443, 1970), by the search for similarity method of Person and Lipman (Proc. Natl. Acad. Sci., *USA* 85:2444, 1988), each of which is incorporated herein by reference; by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI); or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment

programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences.

[0062] A number of genome databases are available for comparison. Several databases containing genomic information annotated with some functional information are maintained by different organizations, and are accessible via the internet, for example, at world wide web addresses (url's) "wwwtigr.org/tdb"; "genetics.wisc.edu"; "genome-www.stanford.edu/~ball"; "hiv-web.lanl.gov"; "ncbi.nlm.nih.gov"; "ebi.ac.uk"; "Pasteur.fr/other/biology"; and "genome.wi.mit.edu".

[0063] In particular, the BLAST and BLAST 2.0 algorithms using default parameters are particularly useful for identifying polynucleotide and polypeptides encompassed within the present invention (Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1977; J. Mol. Biol. 215:403-410, 1990, each of which is incorporated herein by reference). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*, 1977, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the

sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectations (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, Proc. Natl. Acad. Sci., *USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

[0064] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, for example, Karlin and Altschul, Proc. Natl. Acad. Sci., *USA* 90:5873, 1993, which is incorporated herein by reference). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Significantly, upon identifying polynucleotides that are substantially similar to those of SEQ ID NOS:1-5379, the identified polynucleotides can be used as query sequences in a BLAST search to identify polynucleotides and polypeptides substantially similar thereto.

[0065] It should be noted that the nucleotide sequences set forth as SEQ ID NOS:1-2703 comprise coding sequences, whereas the nucleotide sequences set forth as SEQ ID NOS:2704-5379 comprise regulatory sequences. In addition, the coding sequences and regulatory sequences are related in that, for example, SEQ ID NO:1 is the coding sequence of a plant cold regulated gene having a 5' upstream (regulatory) sequence set forth as SEQ ID NO:2704 (see Table 2). Similarly, SEQ ID NO:2705 comprises a regulatory region of SEQ ID NO:2, SEQ ID NO:2706 comprises a regulatory region of SEQ ID NO:3, and so forth as shown in Table 2. As such, reference herein, for example, to a "polynucleotide comprising SEQ ID NO:1" can,

unless indicated otherwise, include at least SEQ ID NO:2704. In some cases, the entire coding region of a plant stress regulated gene or the 5' upstream sequence has not yet been determined (see, for example, SEQ ID NO:43 in Table 3, where "none" indicates that 5' upstream regulatory sequences have not yet been determined). However, the determination of a complete coding sequence where only a portion is known or of regulatory sequences where a portion of the coding sequence is known can be made using methods as disclosed herein or otherwise known in the art.

[0066] In one embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST"). In particular, five specific BLAST programs are used to perform the following task:

(1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

[0067] The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993, each of which is incorporated herein by

reference). Less preferably, the PAM or PAM250 matrices may also be used (Schwartz and Dayhoff, eds., "Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure" (Washington, National Biomedical Research Foundation 1978)). BLAST programs are accessible through the U.S. National Library of Medicine, for example, on the world wide web at address (url) "ncbi.nlm.nih.gov".

[0068] The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some embodiments, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

[0069] The term "substantially similar" also is used in reference to a comparison of expression profiles of nucleotide sequences, wherein a determination that an expression profile characteristic of a stress response is substantially similar to the profile of nucleic acid molecules expressed in a plant cell being examined ("test plant") is indicative of exposure of the test plant cell to one or a combination of abiotic stress conditions. When used in reference to such a comparison of expression profiles, the term "substantially similar" means that that the individual nucleotide sequences in the test plant cell profile are altered in the same manner as the corresponding nucleotide sequences in the expression profile characteristic of the stress response.

[0070] By way of example, where exposure to saline results in an increased expression of nucleotide sequences A, B and C, and a decreased expression of nucleotide sequences D and E, as indicated by the expression profile characteristic of a saline stress response, a determination that corresponding nucleotide sequences A, B and C in the test plant cell are increased and that nucleotides sequences D and E are decreased is indicative of exposure of the test plant cell to a saline stress condition. It should be recognized that, where, for example, only nucleotide sequences A, B, D and E are examined in the test plant cell, an increase in A and B and a decrease in D and E

expression of the test plant cells is considered to be substantially similar to the expression profile characteristic of a saline stress condition and, therefore, is indicative of exposure of the plant cell to a saline stress condition. Similarly, where the levels of expression of the nucleotide sequences examined in a test plant are altered in the same manner, i.e., are increased or are decreased, as that observed in an expression profile characteristic of a particular stress response, the absolute levels of expression may vary, for example, two-fold, five-fold, ten-fold, or the like. Nevertheless, the expression profile of the test plant cell is considered to be substantially similar to the expression profile characteristic of the particular stress response and, therefore, indicative of exposure of the plant cell to the stress condition.

[0071] As disclosed herein, clusters of stress-regulated genes (and their products), some of which also have been described as having cellular functions such as enzymatic activity or roles as transcription factors, are involved in the response of plant cells to various abiotic stresses (see Tables 29-31; see, also, Tables 1 and 32). As such, the polynucleotide sequences comprising the genes in a cluster likely share common stress-regulated regulatory elements, including, for example, cold-regulated regulatory elements (SEQ ID NOS:2704-3955), salinity-regulated regulatory elements (SEQ ID NOS:4910-5107, and osmotic pressure-regulated regulatory elements (SEQ ID NO:5108-5263), as well as regulatory elements that are responsive to a combination of stress conditions, but not to any of the individual stress conditions, alone (SEQ ID NOS:3956-4909 and 5263-5379). The identification of such clusters of genes thus provides a means to identify the stress-regulated regulatory elements that control the level of expression of these genes.

[0072] As used herein, the term "plant stress-regulated gene" means a polynucleotide sequence of a plant, the transcription of which is altered in response to exposure to a stress condition, and the regulatory elements linked to such a polynucleotide sequence and involved in the stress response, which can be induction or repression. In general, plant stress gene regulatory elements are contained within a sequence including approximately two kilobases upstream (5') of the transcription or

translation start site and two kilobases downstream (3') of the transcription or translation termination site. In the absence of an abiotic stress condition, the stress-regulated gene can normally be unexpressed in the cells, can be expressed at a basal level, which is induced to a higher level in response to the stress condition, or can be expressed at a level that is reduced (decreased) in response to the stress condition. The coding region of a plant stress-regulated gene encodes a stress-regulated polypeptide, and also can be the basis for expression of a functional RNA molecule such as an antisense molecule or ribozyme. A stress-regulated polypeptide can have an adaptive effect on a plant, thereby allowing the plant to better tolerate stress conditions; or can have a maladaptive effect, thereby decreasing the ability of the plant to tolerate the stress conditions.

[0073] The present invention provides an isolated plant stress-regulated regulatory element, which regulates expression of an operatively linked nucleotide sequence in a plant in response a stress condition. As disclosed herein, a plant stress-regulated regulatory element can be isolated from a polynucleotide sequence of a plant stress-regulated gene comprising a nucleotide sequence as set forth in SEQ ID NOS:1-2703, for example any of SEQ ID NOS:2704-5379 (see Table 2). It is recognized that certain of the polynucleotides set forth as SEQ ID NOS:1-5379 previously have been described as being involved in a stress-regulated response in plants, including SEQ ID NOS:156, 229, 233, 558, 573, 606, 625, 635, 787, 813, 1263, 1386, 1391, 1405, 1445, 1484, 1589, 1609, 1634, 1726, 1866, 1918, and 1928 and, therefore, are not encompassed, in whole or in part, within the compositions of the invention, and are encompassed within only certain particular methods of the invention, for example, methods of making a transgenic plant that is resistant to two or more stress conditions, since, even where such a gene was known to be expressed in response to a single stress condition such as cold or saline (e.g., SEQ ID NO:1263), it was not known prior to the present disclosure that any of these genes was responsive to a combination of stress conditions (for example, a combination of cold and osmotic stress for SEQ ID NOS:1726, 1866, 1918, and 1928; or a combination of cold, osmotic and saline stress for SEQ ID NOS:1263,1386, 1391, 1405, 1445, 1484, 1589, 1609, and 1634).

[0074] Methods for identifying and isolating the stress-regulated regulatory element from the disclosed polynucleotides, or genomic DNA clones corresponding thereto, are well known in the art. For example, methods of making deletion constructs or linker-scanner constructs can be used to identify nucleotide sequences that are responsive to a stress condition. Generally, such constructs include a reporter gene operatively linked to the sequence to be examined for regulatory activity. By performing such assays, a plant stress-regulated regulatory element can be defined within a sequence of about 500 nucleotides or fewer, generally at least about 200 nucleotides or fewer, particularly about 50 to 100 nucleotides, and more particularly at least about 20 nucleotides or fewer. Preferably the minimal (core) sequence required for regulating a stress response of a plant is identified.

[0075] The nucleotide sequences of the genes of a cluster also can be examined using a homology search engine such as described herein to identify sequences of conserved identity, particularly in the nucleotide sequence upstream of the transcription start site. Since all of the genes in a cluster as disclosed are induced in response to a particular stress condition or a particular combination of stress conditions, some or all of the nucleotide sequences can share conserved stress-regulated regulatory elements. By performing such a homology search, putative stress-regulated regulatory elements can be identified. The ability of such identified sequences to function as a plant stress-regulated regulatory element can be confirmed, for example, by operatively linking the sequence to a reporter gene and assaying the construct for responsiveness to a stress condition.

[0076] As used herein, the term "regulatory element" means a nucleotide sequence that, when operatively linked to a coding region of a gene, effects transcription of the coding region such that a ribonucleic acid (RNA) molecule is transcribed from the coding region. A regulatory element generally can increase or decrease the amount of transcription of a nucleotide sequence, for example, a coding sequence, operatively linked to the element with respect to the level at which the nucleotide sequence would be transcribed absent the regulatory element. Regulatory elements are well known in

the art and include promoters, enhancers, silencers, inactivated silencer intron sequences, 3'-untranslated or 5'-untranslated sequences of transcribed sequence, for example, a poly-A signal sequence, or other protein or RNA stabilizing elements, or other gene expression control elements known to regulate gene expression or the amount of expression of a gene product. A regulatory element can be isolated from a naturally occurring genomic DNA sequence or can be synthetic, for example, a synthetic promoter.

[0077] Regulatory elements can be constitutively expressed regulatory element, which maintain gene expression at a relative level of activity (basal level), or can be regulated regulatory elements. Constitutively expressed regulatory elements can be expressed in any cell type, or can be tissue specific, which are expressed only in particular cell types, phase specific, which are expressed only during particular developmental or growth stages of a plant cell, or the like. A regulatory element such as a tissue specific or phase specific regulatory element or an inducible regulatory element useful in constructing a recombinant polynucleotide or in a practicing a method of the invention can be a regulatory element that generally, in nature, is found in a plant genome. However, the regulatory element also can be from an organism other than a plant, including, for example, from a plant virus, an animal virus, or a cell from an animal or other multicellular organism.

[0078] A regulatory element useful for practicing method of the present is a promoter element. Useful promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, spatially-regulated, chemically regulated, stress-responsive, tissue-specific, viral and synthetic promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level

of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

[0079] Within a plant promoter region there are several domains that are necessary for full function of the promoter. The first of these domains lies immediately upstream of the structural gene and forms the "core promoter region" containing consensus sequences, normally 70 base pairs immediately upstream of the gene. The core promoter region contains the characteristic CAAT and TATA boxes plus surrounding sequences, and represents a transcription initiation sequence that defines the transcription start point for the structural gene.

[0080] The presence of the core promoter region defines a sequence as being a promoter: if the region is absent, the promoter is non-functional. The core promoter region, however, is insufficient to provide full promoter activity. A series of regulatory sequences upstream of the core constitute the remainder of the promoter. These regulatory sequences determine expression level, the spatial and temporal pattern of expression and, for an important subset of promoters, expression under inductive conditions (regulation by external factors such as light, temperature, chemicals, hormones).

[0081] To define a minimal promoter region, a DNA segment representing the promoter region is removed from the 5' region of the gene of interest and operably linked to the coding sequence of a marker (reporter) gene by recombinant DNA techniques well known to the art. The reporter gene is operably linked downstream of the promoter, so that transcripts initiating at the promoter proceed through the reporter gene. Reporter genes generally encode proteins which are easily measured, including, but not limited to, chloramphenicol acetyl transferase (CAT), beta-glucuronidase (GUS), green fluorescent protein (GFP), β-galactosidase (β-GAL), and luciferase.

[0082] The construct containing the reporter gene under the control of the promoter is then introduced into an appropriate cell type by transfection techniques well known to the art. To assay for the reporter protein, cell lysates are prepared and appropriate assays, which are well known in the art, for the reporter protein are performed. For example, if CAT were the reporter gene of choice, the lysates from cells transfected with constructs containing CAT under the control of a promoter under study are mixed with isotopically labeled chloramphenicol and acetyl-coenzyme A (acetyl-CoA). The CAT enzyme transfers the acetyl group from acetyl-CoA to the 2-position or 3-position of chloramphenicol. The reaction is monitored by thin layer chromatography, which separates acetylated chloramphenicol from unreacted material. The reaction products are then visualized by autoradiography.

[0083] The level of enzyme activity corresponds to the amount of enzyme that was made, which in turn reveals the level of expression from the promoter of interest. This level of expression can be compared to other promoters to determine the relative strength of the promoter under study. In order to be sure that the level of expression is determined by the promoter, rather than by the stability of the mRNA, the level of the reporter mRNA can be measured directly, for example, by northern blot analysis.

[0084] Once activity is detected, mutational and/or deletional analyses may be employed to determine the minimal region and/or sequences required to initiate transcription. Thus, sequences can be deleted at the 5' end of the promoter region and/or at the 3' end of the promoter region, and nucleotide substitutions introduced. These constructs are then introduced to cells and their activity determined.

[0085] The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In some cases, expression in multiple tissues is desirable. While in others, tissue-specific, e.g., leaf-specific, seed-specific, petal-specific, anther-specific, or pith-specific, expression is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are

selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. There is, however, no restriction to the origin or source of a selected promoter. It is sufficient that the promoters are operational in driving the expression of a desired nucleotide sequence in the particular cell.

[0086] A range of naturally-occurring promoters are known to be operative in plants and have been used to drive the expression of heterologous (both foreign and endogenous) genes and nucleotide sequences in plants: for example, the constitutive 35S cauliflower mosaic virus (CaMV) promoter, the ripening-enhanced tomato polygalacturonase promoter (Bird et al., 1988), the E8 promoter (Diekman and Fischer, 1988) and the fruit specific 2A1 promoter (Pear et al., 1989). Many other promoters, e.g., U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD zein protein, inducible promoters, such as the light inducible promoter derived from the pea rbcS gene and the actin promoter from rice, e.g., the actin 2 promoter (WO 00/70067); seed specific promoters, such as the phaseolin promoter from beans, may also be used. The nucleotide sequences of the stress-regulated genes of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Chemical induction of gene expression is detailed in EP 0 332 104 and U.S. Pat. 5,614,395.

[0087] In some instances it may be desirable to link a constitutive promoter to a polynucleotide comprising a stress regulated gene of the invention. Examples of some constitutive promoters include the rice actin 1 (Wang et al., 1992; U.S. Pat. No. 5,641,876), CaMV 35S (Odell et al., 1985), CaMV 19S (Lawton et al., 1987), *nos*, Adh, sucrose synthase; and the ubiquitin promoters.

[0088] In other situations it may be desirable to limit expression of stress-related sequences to specific tissues or stages of development. As used herein, the term "tissue specific or phase specific regulatory element" means a nucleotide sequence that effects transcription in only one or a few cell types, or only during one or a few stages of the life cycle of a plant, for example, only for a period of time during a particular stage of growth, development or differentiation. The terms "tissue specific" and "phase specific" are used together herein in referring to a regulatory element because a single regulatory element can have characteristics of both types of regulatory elements. For example, a regulatory element active only during a particular stage of plant development also can be expressed only in one or a few types of cells in the plant during the particular stage of development. As such, any attempt to classify such regulatory elements as tissue specific or as phase specific can be difficult. Accordingly, unless indicated otherwise, all regulatory elements having the characteristic of a tissue specific regulatory element, or a phase specific regulatory element, or both are considered together for purposes of the present invention.

[0089] Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990) corn alcohol dehydrogenase 1 (Vogel et al., 1989; Dennis et al., 1984), corn light harvesting complex (Simpson, 1986; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985), pea small subunit RuBP carboxylase (Poulsen et al., 1986), Ti plasmid mannopine synthase and Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α-tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), histone, and chalcone synthase promoters (Franken et al., 1991). Tissue specific enhancers are described by Fromm et al. (1989).

[0090] Several other tissue-specific regulated genes and/or promoters have been reported in plants, including genes encoding seed storage proteins such as napin, cruciferin, beta-conglycinin, and phaseolin, zein or oil body proteins such as oleosin, genes involved in fatty acid biosynthesis, including acyl carrier protein, stearoyl-ACP desaturase, fatty acid desaturases (fad 2-1), and other genes expressed during embryonic development such as Bce4 (see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific expression is the pea vicilin promoter (Czako et al., 1992). (See also U.S. Pat. No. 5,625,136, which is incorporated herein by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995).

[0091] A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. Pat. No. 4,943,674. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Pat. Nos. 4,535,060, 4,769,061, 4,801,590, and 5,107,065, each of which is incorporated herein by reference.

[0092] Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

[0093] Additional tissue specific or phase specific regulatory elements include, for example, the *AGL8/FRUITFULL* regulatory element, which is activated upon floral

induction (Hempel et al., Development 124:3845-3853, 1997, which is incorporated herein by reference); root specific regulatory elements such as the regulatory elements from the RCP1 gene and the LRP1 gene (Tsugeki and Fedoroff, Proc. Natl. Acad., *USA* 96:12941-12946, 1999; Smith and Fedoroff, Plant Cell 7:735-745, 1995, each of which is incorporated herein by reference); flower specific regulatory elements such as the regulatory elements from the *LEAFY* gene and the *APETELA1* gene (Blazquez et al., Development 124:3835-3844, 1997, which is incorporated herein by reference; Hempel et al., *supra*, 1997); seed specific regulatory elements such as the regulatory element from the oleosin gene (Plant et al., Plant Mol. Biol. 25:193-205, 1994, which is incorporated herein by reference), and dehiscence zone specific regulatory element. Additional tissue specific or phase specific regulatory elements include the Zn13 promoter, which is a pollen specific promoter (Hamilton et al., Plant Mol. Biol. 18:211-218, 1992, which is incorporated herein by reference); the *UNUSUAL FLORAL ORGANS* (*UFO*) promoter, which is active in apical shoot meristem; the promoter active in shoot meristems (Atanassova et al., Plant J. 2:291, 1992, which is incorporated herein by reference), the cdc2a promoter and cyc07 promoter (see, for example, Ito et al., Plant Mol. Biol. 24:863, 1994; Martinez et al., Proc. Natl. Acad. Sci., *USA* 89:7360, 1992; Medford et al., Plant Cell 3:359, 1991; Terada et al., Plant J. 3:241, 1993; Wissenbach et al., Plant J. 4:411, 1993, each of which is incorporated herein by reference); the promoter of the *APETELA3* gene, which is active in floral meristems (Jack et al., Cell 76:703, 1994, which is incorporated herein by reference; Hempel et al., *supra*, 1997); a promoter of an agamous-like (AGL) family member, for example, AGL8, which is active in shoot meristem upon the transition to flowering (Hempel et al., *supra*, 1997); floral abscission zone promoters; L1-specific promoters; and the like.

[0094] The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379).

Several inducible promoters ("gene switches") have been reported, many of which are described in the review by Gatz (1996) and Gatz (1997). These include tetracycline repressor system, *Lac* repressor system, copper inducible systems, salicylate inducible systems (such as the PR1a system), glucocorticoid (Aoyama et al., 1997) and ecdysone inducible systems. Also included are the benzene sulphonamide (U.S. Pat. No. 5,364,780) and alcohol (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters.

[0095] In some instances it might be desirable to inhibit expression of a native DNA sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA sequence.

[0096] Inducible regulatory elements also are useful for purposes of the present invention. As used herein, the term "inducible regulatory element" means a regulatory element that, when exposed to an inducing agent, effects an increased level of transcription of a nucleotide sequence to which it is operatively linked as compared to the level of transcription, if any, in the absence of an inducing agent. Inducible regulatory elements can be those that have no basal or constitutive activity and only effect transcription upon exposure to an inducing agent, or those that effect a basal or constitutive level of transcription, which is increased upon exposure to an inducing agent. Inducible regulatory elements that effect a basal or constitutive level of expression generally are useful in a method or composition of the invention where the induced level of transcription is substantially greater than the basal or constitutive level of expression, for example, at least about two-fold greater, or at least about five-fold greater. Particularly useful inducible regulatory elements do not have a basal or constitutive activity, or increase the level of transcription at least about ten-fold

greater than a basal or constitutive level of transcription associated with the regulatory element.

[0097] Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

[0098] The term "inducing agent" is used to refer to a chemical, biological or physical agent or environmental condition that effects transcription from an inducible regulatory element. In response to exposure to an inducing agent, transcription from the inducible regulatory element generally is initiated *de novo* or is increased above a basal or constitutive level of expression. Such induction can be identified using the methods disclosed herein, including detecting an increased level of RNA transcribed from a nucleotide sequence operatively linked to the regulatory element, increased expression of a polypeptide encoded by the nucleotide sequence, or a phenotype conferred by expression of the encoded polypeptide.

[0099] An inducing agent useful in a method of the invention is selected based on the particular inducible regulatory element. For example, the inducible regulatory element can be a metallothionein regulatory element, a copper inducible regulatory element or a tetracycline inducible regulatory element, the transcription from which can be effected in response to metal ions, copper or tetracycline, respectively (Furst et al., Cell 55:705-717, 1988; Mett et al., Proc. Natl. Acad. Sci., *USA* 90:4567-4571, 1993; Gatz et al., Plant J. 2:397-404, 1992; Roder et al., Mol. Gen. Genet. 243:32-38, 1994, each of which is incorporated herein by reference). The inducible regulatory element also can be an ecdysone regulatory element or a glucocorticoid regulatory element, the transcription from which can be effected in response to ecdysone or other steroid (Christopherson et al., Proc. Natl. Acad. Sci., *USA* 89:6314-6318, 1992;

Schena et al., Proc. Natl. Acad. Sci., *USA* 88:10421-10425, 1991, each of which is incorporated herein by reference). In addition, the regulatory element can be a cold responsive regulatory element or a heat shock regulatory element, the transcription of which can be effected in response to exposure to cold or heat, respectively (Takahashi et al., Plant Physiol. 99:383-390, 1992, which is incorporated herein by reference). Additional regulatory elements useful in the methods or compositions of the invention include, for example, the spinach nitrite reductase gene regulatory element (Back et al., Plant Mol. Biol. 17:9, 1991, which is incorporated herein by reference); a light inducible regulatory element (Feinbaum et al., Mol. Gen. Genet. 226:449, 1991; Lam and Chua, Science 248:471, 1990, each of which is incorporated herein by reference), a plant hormone inducible regulatory element (Yamaguchi-Shinozaki et al., Plant Mol. Biol. 15:905, 1990; Kares et al., Plant Mol. Biol. 15:225, 1990, each of which is incorporated herein by reference), and the like.

[0100] An inducible regulatory element also can be a plant stress-regulated regulatory element of the invention. In addition to the known stress conditions that specifically induce or repress expression from such elements, the present invention provides methods of identifying agents that mimic a stress condition. Accordingly, such stress mimics are considered inducing or repressing agents with respect to a plant stress-regulated regulatory element. In addition, a recombinant polypeptide comprising a zinc finger domain, which is specific for the regulatory element, and an effector domain, particularly an activator, can be useful as an inducing agent for a plant stress-regulated regulatory element. Furthermore, such a recombinant polypeptide provides the advantage that the effector domain can be a repressor domain, thereby providing a repressing agent, which decreases expression from the regulatory element. In addition, use of such a method of modulating expression of an endogenous plant stress-regulated gene provides the advantage that the polynucleotide encoding the recombinant polypeptide can be introduced into cells of the plant, thus providing a transgenic plant that can be regulated coordinately with the endogenous plant stress-regulated gene upon exposure to a stress condition. A polynucleotide encoding such a recombinant polypeptide can be operatively linked to and expressed

from a constitutively active, inducible or tissue specific or phase specific regulatory element.

[0101] In one embodiment, the promoter may be a gamma zein promoter, an oleosin ole16 promoter, a globulin I promoter, an actin I promoter, an actin cl promoter, a sucrose synthetase promoter, an INOPS promoter, an EXM5 promoter, a globulin2 promoter, a b-32, ADPG-pyrophosphorylase promoter, an LtpI promoter, an Ltp2 promoter, an oleosin ole17 promoter, an oleosin ole18 promoter, an actin 2 promoter, a pollen-specific protein promoter, a pollen-specific pectate lyase promoter, an anther-specific protein promoter (Huffman), an anther-specific gene RTS2 promoter, a pollen- specific gene promoter, a tapeturn-specific gene promoter, tapeturn- specific gene RAB24 promoter, a anthranilate synthase alpha subunit promoter, an alpha zein promoter, an anthranilate synthase beta subunit promoter, a dihydrodipicolinate synthase promoter, a Thi l promoter, an alcohol dehydrogenase promoter, a cab binding protein promoter, an H3C4 promoter, a RUBISCO SS starch branching enzyme promoter, an ACCase promoter, an actin3 promoter, an actin7 promoter, a regulatory protein GF14-12 promoter, a ribosomal protein L9 promoter, a cellulose biosynthetic enzyme promoter, an S-adenosyl-L-homocysteine hydrolase promoter, a superoxide dismutase promoter, a C-kinase receptor promoter, a phosphoglycerate mutase promoter, a root-specific RCc3 mRNA promoter, a glucose-6 phosphate isomerase promoter, a pyrophosphate-fructose 6-phosphate-l-phosphotransferase promoter, an ubiquitin promoter, a beta-ketoacyl-ACP synthase promoter, a 33 kDa photosystem 11 promoter, an oxygen evolving protein promoter, a 69 kDa vacuolar ATPase subunit promoter, a metallothionein-like protein promoter, a glyceraldehyde-3-phosphate dehydrogenase promoter, an ABA- and ripening-inducible-like protein promoter, a phenylalanine ammonia lyase promoter, an adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase promoter, an a-tubulin promoter, a cab promoter, a PEPCase promoter, an R gene promoter, a lectin promoter, a light harvesting complex promoter, a heat shock protein promoter, a chalcone synthase promoter, a zein promoter, a globulin-1 promoter, an ABA promoter, an auxin-binding protein promoter, a UDP glucose flavonoid glycosyl-

transferase gene promoter, an NTI promoter, an actin promoter, an opaque 2 promoter, a b70 promoter, an oleosin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a histone promoter, a turgor-inducible promoter, a pea small subunit RuBP carboxylase promoter, a Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, a petunia chalcone isomerase promoter, a bean glycine rich protein I promoter, a CaMV 35S transcript promoter, a potato patatin promoter, or a S-E9 small subunit RuBP carboxylase promoter.

[0102] In addition to promoters, a variety of 5′ and 3′ transcriptional regulatory sequences are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA polyadenylation. The 3'-untranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea rbcS E9 terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3′ end of the protease inhibitor I or II genes from potato or tomato, although other 3′ elements known to those of skill in the art can also be employed. Alternatively, one also could use a gamma coixin, oleosin 3 or other terminator from the genus *Coix*. Preferred 3' elements include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan et al., 1983), the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato.

[0103] As the DNA sequence between the transcription initiation site and the start of the coding sequence, i.e., the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Preferred leader sequences are contemplated to include those that include sequences predicted to direct optimum expression of the attached sequence, i.e., to include a preferred

consensus leader sequence that may increase or maintain mRNA stability and prevent inappropriate initiation of translation. The choice of such sequences will be known to those of skill in the art in light of the present disclosure. Sequences that are derived from genes that are highly expressed in plants will be most preferred.

[0104] Other sequences that have been found to enhance gene expression in transgenic plants include intron sequences (e.g., from *Adh1, bronze1, actin1, actin 2* (WO 00/760067), or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from tobacco mosaic virus (TMV), maize chlorotic mottle virus (MCMV), and alfalfa mosaic virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to picornavirus leaders, for example, EMCV leader (encephalomyocarditis virus 5' non-coding region; Elroy-Stein et al., 1989); potyvirus leaders, for example, TEV leader (tobacco etch virus); MDMV leader (maize dwarf mosaic virus); human immunoglobulin heavy chain binding protein (BiP) leader, (Macejak et al., 1991); untranslated leader from the coat protein mRNA of AMV (AMV RNA 4; Jobling et al., 1987), TMV (Gallie et al., 1989), and MCMV (Lommel et al., 1991; see also, della Cioppa et al., 1987).

[0105] Regulatory elements such as Adh intron 1 (Callis et al., 1987), sucrose synthase intron (Vasil et al., 1989) or TMV omega element (Gallie, et al., 1989), may further be included where desired. Examples of enhancers include elements from the CaMV 35S promoter, octopine synthase genes (Ellis et al., 1987), the rice actin I gene, the maize alcohol dehydrogenase gene (Callis et al., 1987), the maize shrunken I gene (Vasil et al., 1989), TMV Omega element (Gallie et al., 1989) and promoters from non-plant eukaryotes (e.g. yeast; Ma et al., 1988).

[0106] Vectors for use in accordance with the present invention may be constructed to include the ocs enhancer element, which was first identified as a 16 bp

palindromic enhancer from the octopine synthase (ocs) gene of ultilane (Ellis et al., 1987), and is present in at least 10 other promoters (Bouchez et al., 1989). The use of an enhancer element, such as the ocs element and particularly multiple copies of the element, will act to increase the level of transcription from adjacent promoters when applied in the context of monocot transformation.

[0107] The methods of the invention provide genetically modified plant cells, which can contain, for example, a coding region, or peptide portion thereof, of a plant stress-regulated gene operatively linked to a heterologous inducible regulatory element; or a plant stress-regulated regulatory element operatively linked to a heterologous nucleotide sequence encoding a polypeptide of interest. In such a plant, the expression from the inducible regulatory element can be effected by exposing the plant cells to an inducing agent in any of numerous ways depending, for example, on the inducible regulatory element and the inducing agent. For example, where the inducible regulatory element is a cold responsive regulatory element present in the cells of a transgenic plant, the plant can be exposed to cold conditions, which can be produced artificially, for example, by placing the plant in a thermostatically controlled room, or naturally, for example, by planting the plant in an environment characterized, at least in part, by attaining temperatures sufficient to induce transcription from the promoter but not so cold as to kill the plants. By examining the phenotype of such transgenic plants, those plants that ectopically express a gene product that confers increased resistance of the plant to cold can be identified. Similarly, a transgenic plant containing a metallothionein promoter can be exposed to metal ions such as cadmium or copper by watering the plants with a solution containing the inducing metal ions, or can be planted in soil that is contaminated with a level of such metal ions that is toxic to most plants. The phenotype of surviving plants can be observed, those expressing desirable traits can be selected.

[0108] As used herein, the term "phenotype" refers to a physically detectable characteristic. A phenotype can be identified visually by inspecting the physical appearance of a plant following exposure, for example, to increased osmotic

conditions; can be identified using an assay to detecting a product produced due to expression of reporter gene, for example, an RNA molecule, a polypeptide such as an enzyme, or other detectable signal such as disclosed herein; or by using any appropriate tool useful for identifying a phenotype of a plant, for example, a microscope, a fluorescence activated cell sorter, or the like.

[0109] A transgenic plant containing an inducible regulatory element such as a steroid inducible regulatory element can be exposed to a steroid by watering the plants with a solution containing the steroid. The use of an inducible regulatory element that is induced upon exposure to a chemical or biological inducing agent that can be placed in solution or suspension in an aqueous medium can be particularly useful because the inducing agent can be applied conveniently to a relatively large crop of transgenic plants containing the inducible regulatory element, for example, through a watering system or by spraying the inducing agent over the field. As such, inducible regulatory elements that are responsive to an environmental inducing agent, for example, cold; heat; metal ions or other potentially toxic agents such as a pesticides, which can contaminate a soil; or the like; or inducible regulatory elements that are regulated by inducing agents that conveniently can be applied to plants, can be particularly useful in a method or composition of the invention, and allow the identification and selection of plants that express desirable traits and survive and grow in environments that otherwise would not support growth of the plants.

[0110] As disclosed herein, the present invention provides plant stress-regulated regulatory elements, which are identified based on the expression of clusters of plant genes in response to stress. As used herein, the term "stress-regulated regulatory element of a plant" or "plant stress-regulated regulatory element" means a nucleotide sequence of a plant genome that can respond to a stress such that expression of a gene product encoded by a gene comprising the regulatory element (a stress-inducible gene) is increased above or decreased below the level of expression of the gene product in the absence of the stress condition. The regulatory element can be any gene regulatory element, including, for example, a promoter, an enhancer, a silencer,

or the like. In one embodiment, the plant stress-regulated regulatory element is a plant stress-regulated promoter.

[0111] For purposes of modulating the responsiveness of a plant to a stress condition, it can be useful to introduce a modified plant stress-regulated regulatory element into a plant. Such a modified regulatory element can have any desirable characteristic, for example, it can be inducible to a greater level than the corresponding wild-type promoter, or it can be inactivated such that, upon exposure to a stress, there is little or no induction of expression of a nucleotide sequence operatively linked to the mutant element. A plant stress-regulated regulatory element can be modified by incorporating random mutations using, for example, *in vitro* recombination or DNA shuffling (Stemmer et al., Nature 370: 389-391, 1994; U.S. Pat. No. 5,605,793, each of which is incorporated herein by reference). Using such a method, millions of mutant copies of the polynucleotide, for example, stress-regulated regulatory element, can be produced based on the original nucleotide sequence, and variants with improved properties, such as increased inducibility can be recovered.

[0112] A mutation method such as DNA shuffling encompasses forming a mutagenized double-stranded polynucleotide from a template double-stranded polynucleotide, wherein the template double-stranded polynucleotide has been cleaved into double stranded random fragments of a desired size, and comprises the steps of adding to the resultant population of double-stranded random fragments one or more single or double stranded oligonucleotides, wherein the oligonucleotides comprise an area of identity and an area of heterology to the double stranded template polynucleotide; denaturing the resultant mixture of double stranded random fragments and oligonucleotides into single stranded fragments; incubating the resultant population of single stranded fragments with a polymerase under conditions that result in the annealing of the single stranded fragments at the areas of identity to form pairs of annealed fragments, the areas of identity being sufficient for one member of a pair to prime replication of the other, thereby forming a mutagenized double-stranded polynucleotide; and repeating the second and third steps for at least two further

cycles, wherein the resultant mixture in the second step of a further cycle includes the mutagenized double-stranded polynucleotide from the third step of the previous cycle, and the further cycle forms a further mutagenized double-stranded polynucleotide. Preferably, the concentration of a single species of double stranded random fragment in the population of double stranded random fragments is less than 1% by weight of the total DNA. In addition, the template double stranded polynucleotide can comprise at least about 100 species of polynucleotides. The size of the double stranded random fragments can be from about 5 base pairs to 5 kilobase pairs. In a further embodiment, the fourth step of the method comprises repeating the second and the third steps for at least 10 cycles.

[0113] A plant stress-regulated regulatory element of the invention is useful for expressing a nucleotide sequence operatively linked to the element in a cell, particularly a plant cell. As used herein, the term "expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. In the case of an antisense molecule, for example, the term "expression" refers to the transcription of the polynucleotide encoding the antisense molecule.

[0114] As used herein, the term "operatively linked," when used in reference to a plant stress-regulated regulatory element, means that the regulatory element is positioned with respect to a second nucleotide sequence such that the regulatory element effects transcription or transcription and translation of the nucleotide sequence in substantially the same manner, but not necessarily to the same extent, as it does when the regulatory element is present in its natural position in a genome. Transcriptional promoters, for example, generally act in a position and orientation dependent manner and usually are positioned at or within about five nucleotides to about fifty nucleotides 5' (upstream) of the start site of transcription of a gene in nature. In comparison, enhancers and silencers can act in a relatively position or orientation independent manner and, therefore, can be positioned several hundred or thousand nucleotides upstream or downstream from a transcription start site, or in an

intron within the coding region of a gene, yet still be operatively linked to a coding region so as to effect transcription.

[0115] The second nucleotide sequence, i.e., the sequence operatively linked to the plant stress-regulated regulatory element, can be any nucleotide sequence, including, for example, a coding region of a gene or cDNA; a sequence encoding an antisense molecule, an RNAi molecule, ribozyme, triplexing agent (see, for example, Frank-Kamenetskii and Mirkin, Ann. Rev. Biochem. 64:65-95, 1995), or the like; or a sequence that, when transcribed, can be detected in the cell using, for example, by hybridization or amplification, or when translated produces a detectable signal. The term "coding region" is used broadly herein to include a nucleotide sequence of a genomic DNA or a cDNA molecule comprising all or part of a coding region of the coding strand. A coding region can be transcribed from an operatively linked regulatory element, and can be translated into a full length polypeptide or a peptide portion of a polypeptide. It should be recognized that, in a nucleotide sequence comprising a coding region, not all of the nucleotides in the sequence need necessarily encode the polypeptide and, particularly, that a gene transcript can contain one or more introns, which do not encode an amino acid sequence of a polypeptide but, nevertheless, are part of the coding region, particularly the coding strand, of the gene.

[0116] The present invention also relates to a recombinant polynucleotide, which contains a polynucleotide portion of a plant stress-regulated gene operatively linked to a heterologous nucleotide sequence. As used herein, the term "polynucleotide portion of plant stress-regulated sequence" means a contiguous nucleotide sequence of the plant stress-regulated gene that provides a function. The portion can be any portion of the sequence, particularly a coding sequence, or a sequence encoding a peptide portion of the stress-regulated polypeptide; the stress-regulated regulatory element; a sequence useful as an antisense molecule or triplexing agent; or a sequence useful for disrupting (knocking-out) an endogenous plant stress-regulated gene.

[0117] A heterologous nucleotide sequence is a nucleotide sequence that is not normally part of the plant stress-regulated gene from which the polynucleotide portion of the plant stress-regulated gene-component of the recombinant polynucleotide is obtained; or, if it is a part of the plant stress-regulated gene from which the polynucleotide portion is obtained, it is an orientation other than it would normally be in, for example, is an antisense sequence, or comprises at least partially discontinuous as compared to the genomic structure, for example, a single exon operatively linked to the regulatory element. In general, where the polynucleotide portion of the plant stress-regulated gene comprises the coding sequence in a recombinant polynucleotide of the invention, the heterologous nucleotide sequence will function as a regulatory element. The regulatory element can be any heterologous regulatory element, including, for example, a constitutively active regulatory element, an inducible regulatory element, or a tissue specific or phase specific regulatory element, as disclosed above. Conversely, where the polynucleotide portion of the plant stress-regulated polynucleotide comprises the stress-regulated regulatory element of a recombinant polynucleotide of the invention, the heterologous nucleotide sequence generally will be a nucleotide sequence that can be transcribed and, if desired, translated. Where the heterologous nucleotide sequence is expressed from a plant stress-regulated regulatory element, it generally confers a desirable phenotype to a plant cell containing the recombinant polynucleotide, or provides a means to identify a plant cell containing the recombinant polynucleotide. It should be recognized that a "desirable" phenotype can be one that decreases the ability of a plant cell to compete where the plant cell, or a plant containing the cell, is an undesired plant cell. Thus, a heterologous nucleotide sequence can allow a plant to grow, for example, under conditions in which it would not normally be able to grow.

[0118] A heterologous nucleotide sequence can be, or encode, a selectable marker. As used herein, the term "selectable marker" is used herein to refer to a molecule that, when present or expressed in a plant cell, provides a means to identify a plant cell containing the marker. As such, a selectable marker can provide a means for screening a population of plants, or plant cells, to identify those having the marker. A

selectable marker also can confer a selective advantage to the plant cell, or a plant containing the cell. The selective advantage can be, for example, the ability to grow in the presence of a negative selective agent such as an antibiotic or herbicide, compared to the growth of plant cells that do not contain the selectable marker. The selective advantage also can be due, for example, to an enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. A selectable advantage can be conferred, for example, by a single polynucleotide, or its expression product, or to a combination of polynucleotides whose expression in a plant cell gives the cell with a positive selective advantage, a negative selective advantage, or both.

[0119] Examples of selectable markers include those that confer antimetabolite resistance, for example, dihydrofolate reductase, which confers resistance to methotrexate (Reiss, Plant Physiol. (Life Sci. Adv.) 13:143-149, 1994); neomycin phosphotransferase, which confers resistance to the aminoglycosides neomycin, kanamycin and paromycin (Herrera-Estrella, EMBO J. 2:987-995, 1983) and hygro, which confers resistance to hygromycin (Marsh, Gene 32:481-485, 1984), trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman, Proc. Natl. Acad. Sci., *USA* 85:8047, 1988); mannose-6-phosphate isomerase which allows cells to utilize mannose (WO 94/20627); ornithine decarboxylase, which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine (DFMO; McConlogue, 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.); and deaminase from *Aspergillus terreus*, which confers resistance to Blasticidin S (Tamura, Biosci. Biotechnol. Biochem. 59:2336-2338, 1995). Additional selectable markers include those that confer herbicide resistance, for example, phosphinothricin acetyltransferase gene, which confers resistance to phosphinothricin (White et al., Nucl. Acids Res. 18:1062, 1990; Spencer et al., Theor. Appl. Genet. 79:625-631, 1990), a mutant EPSPV-synthase, which confers glyphosate resistance (Hinchee et al., Bio/Technology 91:915-922, 1998), a mutant acetolactate synthase, which confers imidazolione or sulfonylurea resistance (Lee et al., EMBO J. 7:1241-1248, 1988), a mutant psbA, which confers resistance to atrazine (Smeda et

al., Plant Physiol. 103:911-917, 1993), or a mutant protoporphyrinogen oxidase (see U.S. Pat. No. 5,767,373), or other markers conferring resistance to an herbicide such as glufosinate. In addition, markers that facilitate identification of a plant cell containing the polynucleotide encoding the marker include, for example, luciferase (Giacomin, Plant Sci. 116:59-72, 1996; Scikantha, J. Bacteriol. 178:121, 1996), green fluorescent protein (Gerdes, FEBS Lett. 389:44-47, 1996) or fl-glucuronidase (Jefferson, EMBO J. 6:3901-3907, 1997), and numerous others as disclosed herein or otherwise known in the art. Such markers also can be used as reporter molecules.

[0120] A heterologous nucleotide sequence can encode an antisense molecule, particularly an antisense molecule specific for a nucleotide sequence of a plant stress-regulated gene, for example, the gene from which the regulatory component of the recombinant polynucleotide is derived. Such a recombinant polynucleotide can be useful for reducing the expression of a plant stress-regulated polypeptide in response to a stress condition because the antisense molecule, like the polypeptide, only will be induced upon exposure to the stress. A heterologous nucleotide sequence also can be, or can encode, a ribozyme or a triplexing agent. In addition to being useful as heterologous nucleotide sequences, such molecules also can be used directly in a method of the invention, for example, to modulate the responsiveness of a plant cell to a stress condition. Thus, an antisense molecule, ribozyme, or triplexing agent can be contacted directly with a target cell and, upon uptake by the cell, can effect their antisense, ribozyme or triplexing activity; or can be encoded by a heterologous nucleotide sequence that is expressed in a plant cell from a plant stress-regulated regulatory element, whereupon it can effect its activity.

[0121] An antisense polynucleotide, ribozyme or triplexing agent is complementary to a target sequence, which can be a DNA or RNA sequence, for example, messenger RNA, and can be a coding sequence, a nucleotide sequence comprising an intron-exon junction, a regulatory sequence such as a Shine-Delgarno-like sequence, or the like. The degree of complementarity is such that the polynucleotide, for example, an antisense polynucleotide, can interact specifically

with the target sequence in a cell. Depending on the total length of the antisense or other polynucleotide, one or a few mismatches with respect to the target sequence can be tolerated without losing the specificity of the polynucleotide for its target sequence. Thus, few if any mismatches would be tolerated in an antisense molecule consisting, for example, of twenty nucleotides, whereas several mismatches will not affect the hybridization efficiency of an antisense molecule that is complementary, for example, to the full length of a target mRNA encoding a cellular polypeptide. The number of mismatches that can be tolerated can be estimated, for example, using well known formulas for determining hybridization kinetics (see Sambrook et al., "Molecular Cloning; A Laboratory Manual" 2nd Edition (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; 1989)) or can be determined empirically using methods as disclosed herein or otherwise known in the art, particularly by determining that the presence of the antisense polynucleotide, ribozyme, or triplexing agent in a cell decreases the level of the target sequence or the expression of a polypeptide encoded by the target sequence in the cell.

[0122] A nucleotide sequence useful as an antisense molecule, a ribozyme or a triplexing agent can inhibit translation or cleave a polynucleotide encoded by plant stress-regulated gene, thereby modulating the responsiveness of a plant cell to a stress condition. An antisense molecule, for example, can bind to an mRNA to form a double stranded molecule that cannot be translated in a cell. Antisense oligonucleotides of at least about 15 to 25 nucleotides are preferred since they are easily synthesized and can hybridize specifically with a target sequence, although longer antisense molecules can be expressed from a recombinant polynucleotide introduced into the target cell. Specific nucleotide sequences useful as antisense molecules can be identified using well known methods, for example, gene walking methods (see, for example, Seimiya et al., J. Biol. Chem. 272:4631-4636 (1997), which is incorporated herein by reference). Where the antisense molecule is contacted directly with a target cell, it can be operatively associated with a chemically reactive group such as iron-linked EDTA, which cleaves a target RNA at the site of

hybridization. A triplexing agent, in comparison, can stall transcription (Maher et al., Antisense Res. Devel. 1:227 (1991); Helene, Anticancer Drug Design 6:569 (1991)).

[0123] A plant stress-regulated regulatory element can be included in an expression cassette. As used herein, the term "expression cassette" refers to a nucleotide sequence that can direct expression of an operatively linked polynucleotide. Thus, a plant stress-regulated regulatory element can constitute an expression cassette, or component thereof. An expression cassette is particularly useful for directing expression of a nucleotide sequence, which can be an endogenous nucleotide sequence or a heterologous nucleotide sequence, in a cell, particularly a plant cell. If desired, an expression cassette also can contain additional regulatory elements, for example, nucleotide sequences required for proper translation of a polynucleotide sequence into a polypeptide. In general, an expression cassette can be introduced into a plant cell such that the plant cell, a plant resulting from the plant cell, seeds obtained from such a plant, or plants produced from such seeds are resistant to a stress condition.

[0124] Additional regulatory sequences as disclosed above or other desirable sequences such as selectable markers or the like can be incorporated into an expression cassette containing a plant stress-regulated regulatory element (see, for example, WO 99/47552). Examples of suitable markers include dihydrofolate reductase (DHFR) or neomycin resistance for eukaryotic cells and tetracycline or ampicillin resistance for E. coli. Selection markers in plants include bleomycin, gentamycin, glyphosate, hygromycin, kanamycin, methotrexate, phleomycin, phosphinotricin, spectinomycin, streptomycin, sulfonamide and sulfonylureas resistance (see, for example, Maliga et al., *Methods in Plant Molecular Biology*, Cold Spring Harbor Laboratory Press, 1995, page 39). The selection marker can have its own promoter or its expression can be driven by the promoter operably linked to the sequence of interest. Additional sequences such as intron sequences (e.g. from Adh1 or bronze1) or viral leader sequences (e.g. from TMV, MCMV and AIVIV), all of which can enhance expression, can be included in the cassette. In addition, where it is

desirable to target expression of a nucleotide sequence operatively linked to the stress-regulated regulatory element, a sequence encoding a cellular localization motif can be included in the cassette, for example, such that an encoded transcript or translation product is translocated to and localizes in the cytosol, nucleus, a chloroplast, or another subcellular organelle. Examples of useful transit peptides and transit peptide sequences can be found in Von Heijne et al., Plant Mol. Biol. Rep. 9: 104, 1991; Clark et al., J. Biol. Chem. 264:17544, 1989; della Cioppa et al., Plant Physiol. 84:965, 1987; Romer et al., Biochem. Biophys. Res. Comm. 196:1414, 1993; Shah et al., Science 233:478, 1986; Archer et al., J. Bioenerg Biomemb. 22:789, 1990; Scandalios, Prog. Clin. Biol. Res. 344:515, 1990; Weisbeek et al., J. Cell Sci. Suppl. 11:199, 1989; Bruce, Trends Cell Biol. 10:440, 2000. The present invention can utilize native or heterologous transit peptides. The encoding sequence for a transit peptide can include all or a portion of the encoding sequence for a particular transit peptide, and may also contain portions of the mature protein encoding sequence associated with a particular transit peptide.

[0125] A polynucleotide portion of a plant stress-regulated plant gene, or an expression cassette, can be introduced into a cell as a naked DNA molecule, can be incorporated in a matrix such as a liposome or a particle such as a viral particle, or can be incorporated into a vector. Such vectors can be cloning or expression vectors, but other uses are within the scope of the present invention. A cloning vector is a self-replicating DNA molecule that serves to transfer a DNA segment into a host cell. The three most common types of cloning vectors are bacterial plasmids, phages, and other viruses. An expression vector is a cloning vector designed so that a coding sequence inserted at a particular site will be transcribed and translated into a protein. Incorporation of the polynucleotide into a vector can facilitate manipulation of the polynucleotide, or introduction of the polynucleotide into a plant cell. A vector can be derived from a plasmid or a viral vector such as a T-DNA vector (Horsch et al., Science 227:1229-1231, 1985, which is incorporated herein by reference). If desired, the vector can comprise components of a plant transposable element, for example, a Ds transposon (Bancroft and Dean, Genetics 134:1221-1229, 1993, which is

incorporated herein by reference) or an Spm transposon (Aarts et al., Mol. Gen. Genet. 247:555-564, 1995, which is incorporated herein by reference).

[0126] In addition to containing the polynucleotide portion of a plant stress-regulated gene, a vector can contain various nucleotide sequences that facilitate, for example, rescue of the vector from a transformed plant cell; passage of the vector in a host cell, which can be a plant, animal, bacterial, or insect host cell; or expression of an encoding nucleotide sequence in the vector, including all or a portion of a rescued coding region. As such, the vector can contain any of a number of additional transcription and translation elements, including constitutive and inducible promoters, enhancers, and the like (see, for example, Bitter et al., Meth. Enzymol. 153:516-544, 1987). For example, a vector can contain elements useful for passage, growth or expression in a bacterial system, including a bacterial origin of replication; a promoter, which can be an inducible promoter; and the like. In comparison, a vector that can be passaged in a mammalian host cell system can have a promoter such as a metallothionein promoter, which has characteristics of both a constitutive promoter and an inducible promoter, or a viral promoter such as a retrovirus long terminal repeat, an adenovirus late promoter, or the like. A vector also can contain one or more restriction endonuclease recognition and cleavage sites, including, for example, a polylinker sequence, to facilitate rescue of a nucleotide sequence operably linked to the polynucleotide portion.

[0127] The present invention also relates to a method of using a polynucleotide portion of a plant stress-regulated gene to confer a selective advantage on a plant cell. Such a method can be performed by introducing, for example, a plant stress-regulated regulatory element into a plant cell, wherein, upon exposure of the plant cell to a stress condition to which the regulatory element is responsive, a nucleotide sequence operatively linked to the regulatory element is expressed, thereby conferring a selective advantage to plant cell. The operatively linked nucleotide sequence can be a heterologous nucleotide sequence, which can be operatively linked to the regulatory element prior to introduction of the regulatory sequence into the plant cell; or can be

an endogenous nucleotide sequence into which the regulatory element was targeted by a method such as homologous recombination. The selective advantage conferred by the operatively linked nucleotide sequence can be such that the plant is better able to tolerate the stress condition; or can be any other selective advantage.

[0128] As used herein, the term "selective advantage" refers to the ability of a particular organism to better propagate, develop, grow, survive, or otherwise tolerate a condition as compared to a corresponding reference organism that does not contain a plant-stress regulated polynucleotide portion of the present invention. In one embodiment, a selective advantage is exemplified by the ability of a desired plant, plant cell, or the like, that contains an introduced plant stress-regulated regulatory element, to grow better than an undesired plant, plant cell, or the like, that does not contain the introduced regulatory element. For example, a recombinant polynucleotide comprising a plant stress-regulated regulatory element operatively linked to a heterologous nucleotide sequence encoding an enzyme that inactivates an herbicide can be introduced in a desired plant. Upon exposure of a mixed population of plants comprising the desired plants, which contain the recombinant polynucleotide, and one or more other populations of undesired plants, which lack the recombinant polynucleotide, to a stress condition that induces expression of the regulatory element and to the herbicide, the desired plants will have a greater likelihood of surviving exposure to the toxin and, therefore, a selective advantage over the undesired plants.

[0129] In another embodiment, a selective advantage is exemplified by the ability of a desired plant, plant cell, or the like, to better propagate, develop, grow, survive, or otherwise tolerate a condition as compared to an undesired plant, plant cell, or the like, that contains an introduced plant stress-regulated regulatory element. For example, a recombinant polynucleotide comprising a plant stress-regulated regulatory element operatively linked to a plant cell toxin can be introduced into cells of an undesirable plant present in a mixed population of desired and undesired plants, for example, food crops and weeds, respectively, then the plants can be exposed to stress

conditions that induce expression from the plant stress-regulated regulatory element, whereby expression of the plant cell toxin results in inhibition of growth or death of the undesired plants, thereby providing a selective advantage to the desired plants, which no longer have to compete with the undesired plants for nutrients, light, or the like. In another example, a plant stress-regulated regulatory element operatively linked to a plant cell toxin can be introduced into cells of plants used as a nurse crop. Nurse crops, also called cover or companion crops, are planted in combination with plants of interest to provide, among other things, shade and soil stability during establishment of the desired plants. Once the desired plants have become established, the presence of the nurse crop may no longer be desirable. Exposure to conditions inducing expression of the gene linked to the plant stress-regulated regulatory element allows elimination of the nurse crop. Alternatively nurse crops can be made less tolerate to abiotic stress by the inhibition of any of the stress-regulated sequences disclosed herein. Inhibition can be accomplished by any of the method described herein. Upon exposure of the nurse crop to the stress, the decreased ability of the nurse crop to respond to the stress will result in elimination of the nurse crop, leaving only the desired plants.

[0130] The invention also provides a means of producing a transgenic plant, which comprises plant cells that exhibit altered responsiveness to a stress condition. As such, the present invention further provides a transgenic plant, or plant cells or tissues derived therefrom, which are genetically modified to respond to stress differently than a corresponding wild-type plant or plant not containing constructs of the present invention would respond. As used herein, the term "responsiveness to a stress condition" refers to the ability of a plant to express a plant stress-regulated gene upon exposure to the stress condition. A transgenic plant cell contains a polypeptide portion of a plant stress-regulated gene, or a mutant form thereof, for example, a knock-out mutant. A knock-out mutant form of a plant stress-regulated gene can contain, for example, a mutation such that a STOP codon is introduced into the reading frame of the translated portion of the gene such that expression of a functional stress-regulated polypeptide is prevented; or a mutation in the stress-regulated

regulatory element such that inducibility of the element in response to a stress condition is inhibited. Such transgenic plants of the invention can display any of various idiotypic modifications is response to an abiotic stress, including altered tolerance to the stress condition, as well as increased or decreased plant growth, root growth, yield, or the like, as compared to the corresponding wild-type plant.

[0131] The term "plant" is used broadly herein to include any plant at any stage of development, or to part of a plant, including a plant cutting, a plant cell, a plant cell culture, a plant organ, a plant seed, and a plantlet. A plant cell is the structural and physiological unit of the plant, comprising a protoplast and a cell wall. A plant cell can be in the form of an isolated single cell or a cultured cell, or can be part of higher organized unit, for example, a plant tissue, plant organ, or plant. Thus, a plant cell can be a protoplast, a gamete producing cell, or a cell or collection of cells that can regenerate into a whole plant. As such, a seed, which comprises multiple plant cells and is capable of regenerating into a whole plant, is considered plant cell for purposes of this disclosure. A plant tissue or plant organ can be a seed, protoplast, callus, or any other groups of plant cells that is organized into a structural or functional unit. Particularly useful parts of a plant include harvestable parts and parts useful for propagation of progeny plants. A harvestable part of a plant can be any useful part of a plant, for example, flowers, pollen, seedlings, tubers, leaves, stems, fruit, seeds, roots, and the like. A part of a plant useful for propagation includes, for example, seeds, fruits, cuttings, seedlings, tubers, rootstocks, and the like.

[0132] A transgenic plant can be regenerated from a transformed plant cell. As used herein, the term "regenerate" means growing a whole plant from a plant cell; a group of plant cells; a protoplast; a seed; or a piece of a plant such as a callus or tissue. Regeneration from protoplasts varies from species to species of plants. For example, a suspension of protoplasts can be made and, in certain species, embryo formation can be induced from the protoplast suspension, to the stage of ripening and germination. The culture media generally contains various components necessary for growth and regeneration, including, for example, hormones such as auxins and

cytokinins; and amino acids such as glutamic acid and proline, depending on the particular plant species. Efficient regeneration will depend, in part, on the medium, the genotype, and the history of the culture. If these variables are controlled, however, regeneration is reproducible.

[0133] Regeneration can occur from plant callus, explants, organs or plant parts. Transformation can be performed in the context of organ or plant part regeneration. (see Meth. Enzymol. Vol. 118; Klee et al. Ann. Rev. Plant Physiol. 38:467, 1987, which is incorporated herein by reference). Utilizing the leaf disk-transformation-regeneration method, for example, disks are cultured on selective media, followed by shoot formation in about two to four weeks (see Horsch et al., *supra*, 1985). Shoots that develop are excised from calli and transplanted to appropriate root-inducing selective medium. Rooted plantlets are transplanted to soil as soon as possible after roots appear. The plantlets can be repotted as required, until reaching maturity.

[0134] In vegetatively propagated crops, the mature transgenic plants are propagated utilizing cuttings or tissue culture techniques to produce multiple identical plants. Selection of desirable transgenotes is made and new varieties are obtained and propagated vegetatively for commercial use. In seed propagated crops, the mature transgenic plants can be self crossed to produce a homozygous inbred plant. The resulting inbred plant produces seeds that contain the introduced plant stress-induced regulatory element, and can be grown to produce plants that express a polynucleotide or polypeptide in response to a stress condition that induces expression from the regulatory element. As such, the invention further provides seeds produced by a transgenic plant obtained by a method of the invention.

[0135] In addition, transgenic plants comprising different recombinant sequences can be crossbred, thereby providing a means to obtain transgenic plants containing two or more different transgenes, each of which contributes a desirable characteristic to the plant. Methods for breeding plants and selecting for crossbred plants having desirable characteristics or other characteristics of interest are well known in the art.

[0136] A method of the invention can be performed by introducing a polynucleotide portion of a plant stress-regulated gene into the plant. As used herein, the term "introducing" means transferring a polynucleotide into a plant cell. A polynucleotide can be introduced into a cell by a variety of methods well known to those of ordinary skill in the art. For example, the polynucleotide can be introduced into a plant cell using a direct gene transfer method such as electroporation or microprojectile mediated transformation, or using *Agrobacterium* mediated transformation. Non-limiting examples of methods for the introduction of polynucleotides into plants are provided in greater detail herein. As used herein, the term "transformed" refers to a plant cell containing an exogenously introduced polynucleotide portion of a plant stress-regulated gene that is or can be rendered active in a plant cell, or to a plant comprising a plant cell containing such a polynucleotide.

[0137] It should be recognized that one or more polynucleotides, which are the same or different can be introduced into a plant, thereby providing a means to obtain a genetically modified plant containing multiple copies of a single transgenic sequence, or containing two or more different transgenic sequences, either or both of which can be present in multiple copies. Such transgenic plants can be produced, for example, by simply selecting plants having multiple copies of a single type of transgenic sequence; by cotransfecting plant cells with two or more populations of different transgenic sequences and identifying those containing the two or more different transgenic sequences; or by crossbreeding transgenic plants, each of which contains one or more desired transgenic sequences, and identifying those progeny having the desired sequences.

[0138] Methods for introducing a polynucleotide into a plant cell to obtain a transformed plant also include direct gene transfer (see European Patent A 164 575), injection, electroporation, biolistic methods such as particle bombardment, pollen-mediated transformation, plant RNA virus-mediated transformation, liposome-mediated transformation, transformation using wounded or enzyme-degraded

immature embryos, or wounded or enzyme-degraded embryogenic callus, and the like. Transformation methods using *Agrobacterium tumefaciens* tumor inducing (Ti) plasmids or root-inducing (Ri) plasmids, or plant virus vectors are well known in the art (see, for example, WO 99/47552; Weissbach & Weissbach, "Methods for Plant Molecular Biology" (Academic Press, NY 1988), section VIII, pages 421-463; Grierson and Corey, "Plant Molecular Biology" 2d Ed. (Blackie, London 1988), Chapters 7-9, each of which is incorporated herein by reference; Horsch et al., *supra*, 1985). The wild-type form of *Agrobacterium*, for example, contains a Ti plasmid, which directs production of tumorigenic crown gall growth on host plants. Transfer of the tumor inducing T-DNA region of the Ti plasmid to a plant genome requires the Ti plasmid-encoded virulence genes as well as T-DNA borders, which are a set of direct DNA repeats that delineate the region to be transferred. An *Agrobacterium* based vector is a modified form of a Ti plasmid, in which the tumor inducing functions are replaced by a nucleotide sequence of interest that is to be introduced into the plant host.

[0139] Methods of using *Agrobacterium* mediated transformation include cocultivation of *Agrobacterium* with cultured isolated protoplasts; transformation of plant cells or tissues with *Agrobacterium*; and transformation of seeds, apices or meristems with *Agrobacterium*. In addition, *in planta* transformation by *Agrobacterium* can be performed using vacuum infiltration of a suspension of *Agrobacterium* cells (Bechtold et al., C.R. Acad. Sci. Paris 316:1194, 1993, which is incorporated herein by reference).

[0140] *Agrobacterium* mediated transformation can employ cointegrate vectors or binary vector systems, in which the components of the Ti plasmid are divided between a helper vector, which resides permanently in the *Agrobacterium* host and carries the virulence genes, and a shuttle vector, which contains the gene of interest bounded by T-DNA sequences. Binary vectors are well known in the art (see, for example, De Framond, BioTechnology 1:262, 1983; Hoekema et al., Nature 303:179, 1983, each of which is incorporated herein by reference) and are commercially

available (Clontech; Palo Alto CA). For transformation, *Agrobacterium* can be cocultured, for example, with plant cells or wounded tissue such as leaf tissue, root explants, hypocotyledons, stem pieces or tubers (see, for example, Glick and Thompson, "Methods in Plant Molecular Biology and Biotechnology" (Boca Raton FL, CRC Press 1993), which is incorporated herein by reference). Wounded cells within the plant tissue that have been infected by *Agrobacterium* can develop organs *de novo* when cultured under the appropriate conditions; the resulting transgenic shoots eventually give rise to transgenic plants, which contain an exogenous polynucleotide portion of a plant stress-regulated gene.

[0141] *Agrobacterium* mediated transformation has been used to produce a variety of transgenic plants, including, for example, transgenic cruciferous plants such as *Arabidopsis*, mustard, rapeseed and flax; transgenic leguminous plants such as alfalfa, pea, soybean, trefoil and white clover; and transgenic solanaceous plants such as eggplant, petunia, potato, tobacco and tomato (see, for example, Wang et al., "Transformation of Plants and Soil Microorganisms" (Cambridge, University Press 1995), which is incorporated herein by reference). In addition, *Agrobacterium* mediated transformation can be used to introduce an exogenous polynucleotide sequence, for example, a plant stress-regulated regulatory element into apple, aspen, belladonna, black currant, carrot, celery, cotton, cucumber, grape, horseradish, lettuce, morning glory, muskmelon, neem, poplar, strawberry, sugar beet, sunflower, walnut, asparagus, rice and other plants (see, for example, Glick and Thompson, *supra,* 1993; Hiei et al., Plant J. 6:271-282, 1994; Shimamoto, Science 270:1772-1773, 1995).

[0142] Suitable strains of *Agrobacterium tumefaciens* and vectors as well as transformation of Agrobacteria and appropriate growth and selection media are well known in the art (GV3101, pMK90RK), Koncz, Mol. Gen. Genet. 204:383-396, 1986; (C58C1, pGV3850kan), Deblaere, Nucl. Acid Res. 13:4777, 1985; Bevan, Nucl. Acid Res. 12:8711, 1984; Koncz, Proc. Natl. Acad. Sci. *USA* 86:8467-8471, 1986; Koncz, Plant Mol. Biol. 20:963-976, 1992; Koncz, Specialized vectors for gene tagging and expression studies. In: Plant Molecular Biology Manual Vol. 2, Gelvin and

Schilperoort (Eds.), Dordrecht, The Netherlands: Kluwer Academic Publ. (1994), 1-22; European Patent A-1 20 516; Hoekema: The Binary Plant Vector System, Offsetdrukkerij Kanters B. V., Alblasserdam (1985), Chapter V; Fraley, Crit. Rev. Plant. Sci., 4:1-46; An, EMBO J. 4:277-287, 1985).

[0143] Where a polynucleotide portion of a plant stress-regulated gene is contained in vector, the vector can contain functional elements, for example "left border" and "right border" sequences of the T-DNA of *Agrobacterium*, which allow for stable integration into a plant genome. Furthermore, methods and vectors that permit the generation of marker-free transgenic plants, for example, where a selectable marker gene is lost at a certain stage of plant development or plant breeding, are known, and include, for example, methods of co-transformation (Lyznik, Plant Mol. Biol. 13:151-161, 1989; Peng, Plant Mol. Biol. 27:91-104, 1995), or methods that utilize enzymes capable of promoting homologous recombination in plants (see, e.g., W097/08331; Bayley, Plant Mol. Biol. 18:353-361, 1992; Lloyd, Mol. Gen. Genet. 242:653-657, 1994; Maeser, Mol. Gen. Genet. 230:170-176, 1991; Onouchi, Nucl. Acids Res. 19:6373-6378, 1991; see, also, Sambrook et al., *supra*, 1989).

[0144] A direct gene transfer method such as electroporation also can be used to introduce a polynucleotide portion of a plant stress-regulated gene into a cell such as a plant cell. For example, plant protoplasts can be electroporated in the presence of the regulatory element, which can be in a vector (Fromm et al., Proc. Natl. Acad. Sci., *USA* 82:5824, 1985, which is incorporated herein by reference). Electrical impulses of high field strength reversibly permeabilize membranes allowing the introduction of the nucleic acid. Electroporated plant protoplasts reform the cell wall, divide and form a plant callus. Microinjection can be performed as described in Potrykus and Spangenberg (eds.), Gene Transfer To Plants (Springer Verlag, Berlin, NY 1995). A transformed plant cell containing the introduced polynucleotide can be identified by detecting a phenotype due to the introduced polynucleotide, for example, increased or decreased tolerance to a stress condition.

[0145] Microprojectile mediated transformation also can be used to introduce a polynucleotide into a plant cell (Klein et al., Nature 327:70-73, 1987, which is incorporated herein by reference). This method utilizes microprojectiles such as gold or tungsten, which are coated with the desired nucleic acid molecule by precipitation with calcium chloride, spermidine or polyethylene glycol. The microprojectile particles are accelerated at high speed into a plant tissue using a device such as the BIOLISTIC PD-1000 (BioRad; Hercules CA).

[0146] Microprojectile mediated delivery ("particle bombardment") is especially useful to transform plant cells that are difficult to transform or regenerate using other methods. Methods for the transformation using biolistic methods are well known (Wan, Plant Physiol. 104:37-48, 1984; Vasil, Bio/Technology 11:1553-1558, 1993; Christou, Trends in Plant Science 1:423-431, 1996). Microprojectile mediated transformation has been used, for example, to generate a variety of transgenic plant species, including cotton, tobacco, corn, hybrid poplar and papaya (see Glick and Thompson, *supra,* 1993). Important cereal crops such as wheat, oat, barley, sorghum and rice also have been transformed using microprojectile mediated delivery (Duan et al., Nature Biotech. 14:494-498, 1996; Shimamoto, Curr. Opin. Biotech. 5:158-162, 1994). A rapid transformation regeneration system for the production of transgenic plants such as a system that produces transgenic wheat in two to three months (see European Patent No. EP 0709462A2, which is incorporated herein by reference) also can be useful for producing a transgenic plant using a method of the invention, thus allowing more rapid identification of gene functions. The transformation of most dicotyledonous plants is possible with the methods described above. Transformation of monocotyledonous plants also can be transformed using, for example, biolistic methods as described above, protoplast transformation, electroporation of partially permeabilized cells, introduction of DNA using glass fibers, *Agrobacterium* mediated transformation, and the like.

[0147] Plastid transformation also can be used to introduce a polynucleotide portion of a plant stress-regulated gene into a plant cell (U.S. Patent Nos. 5,451,513,

5,545,817, and 5,545,818; WO 95/16783; McBride et al., Proc. Natl. Acad. Sci., *USA* 91:7301-7305, 1994). Chloroplast transformation involves introducing regions of cloned plastid DNA flanking a desired nucleotide sequence, for example, a selectable marker together with polynucleotide of interest into a suitable target tissue, using, for example, a biolistic or protoplast transformation method (e.g., calcium chloride or PEG mediated transformation). One to 1.5 kb flanking regions ("targeting sequences") facilitate homologous recombination with the plastid genome, and allow the replacement or modification of specific regions of the plastome. Using this method, point mutations in the chloroplast 16S rRNA and rps12 genes, which confer resistance to spectinomycin and streptomycin, can be utilized as selectable markers for transformation (Svab et al., Proc. Natl. Acad. Sci., *USA* 87:8526-8530, 1990; Staub and Maliga, Plant Cell 4:39-45, 1992), resulted in stable homopiasmic transformants; at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub and Maliga, EMBO J. 12:601-606, 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial aadA gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransf erase (Svab and Maliga, Proc. Natl. Acad. Sci., *USA* 90:913-917, 1993). Approximately 15 to 20 cell division cycles following transformation are generally required to reach a homoplastidic state. Plastid expression, in which genes are inserted by homologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein.

[0148] Plants suitable to treatment according to a method of the invention can be monocots or dicots and include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale*

cereale), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea ultilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*).

[0149] Ornamentals such as azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum are also included. Additional ornamentals within the scope of the invention include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

[0150] Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey

pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga ultilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*).

[0151] Leguminous plants which may be used in the practice of the present invention include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

[0152] Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, ultilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, ultilane, chicory, groundnut and zucchini.

[0153] Angiosperms are divided into two broad classes based on the number of cotyledons, which are seed leaves that generally store or absorb food; a monocotyledonous angiosperm has a single cotyledon, and a dicotyledonous

angiosperm has two cotyledons. Angiosperms produce a variety of useful products including materials such as lumber, rubber, and paper; fibers such as cotton and linen; herbs and medicines such as quinine and vinblastine; ornamental flowers such as roses and orchids; and foodstuffs such as grains, oils, fruits and vegetables.

[0154] Angiosperms encompass a variety of flowering plants, including, for example, cereal plants, leguminous plants, oilseed plants, hardwood trees, fruit-bearing plants and ornamental flowers, which general classes are not necessarily exclusive. Cereal plants, which produce an edible grain cereal, include, for example, corn, rice, wheat, barley, oat, rye, orchardgrass, guinea grass, sorghum and turfgrass. Leguminous plants include members of the pea family (*Fabaceae*) and produce a characteristic fruit known as a legume. Examples of leguminous plants include, for example, soybean, pea, chickpea, moth bean, broad bean, kidney bean, lima bean, lentil, cowpea, dry bean, and peanut, as well as alfalfa, birdsfoot trefoil, clover and sainfoin. Oilseed plants, which have seeds that are useful as a source of oil, include soybean, sunflower, rapeseed (canola) and cottonseed.

[0155] Angiosperms also include hardwood trees, which are perennial woody plants that generally have a single stem (trunk). Examples of such trees include alder, ash, aspen, basswood (linden), beech, birch, cherry, cottonwood, elm, eucalyptus, hickory, locust, maple, oak, persimmon, poplar, sycamore, walnut, sequoia, and willow. Trees are useful, for example, as a source of pulp, paper, structural material and fuel.

[0156] Angiosperms are fruit-bearing plants that produce a mature, ripened ovary, which generally contains seeds. A fruit can be suitable for human or animal consumption or for collection of seeds to propagate the species. For example, hops are a member of the mulberry family that are prized for their flavoring in malt liquor. Fruit-bearing angiosperms also include grape, orange, lemon, grapefruit, avocado, date, peach, cherry, olive, plum, coconut, apple and pear trees and blackberry, blueberry, raspberry, strawberry, pineapple, tomato, cucumber and eggplant plants.

An ornamental flower is an angiosperm cultivated for its decorative flower. Examples of commercially important ornamental flowers include rose, orchid, lily, tulip and chrysanthemum, snapdragon, camellia, carnation and petunia plants. The skilled artisan will recognize that the methods of the invention can be practiced using these or other angiosperms, as desired, as well as gymnosperms, which do not produce seeds in a fruit.

[0157] A method of producing a transgenic plant can be performed by introducing a polynucleotide portion of plant stress-regulated gene into a plant cell genome, whereby the polynucleotide portion of the plant stress-regulated gene modulates a response of the plant cell to a stress condition, thereby producing a transgenic plant, which comprises plant cells that exhibit altered responsiveness to the stress condition. In one embodiment, the polynucleotide portion of the plant stress-regulated gene encodes a stress-regulated polypeptide or functional peptide portion thereof, wherein expression of the stress-regulated polypeptide or functional peptide portion thereof either increases the stress tolerance of the transgenic plant, or decreases the stress tolerance of the transgenic plant. The polynucleotide portion of the plant stress-regulated gene encoding the stress-regulated polypeptide or functional peptide portion thereof can be operatively linked to a heterologous promoter.

[0158] In another embodiment, the polynucleotide portion of the plant stress-regulated gene comprises a stress-regulated regulatory element. The stress-regulated regulatory element can integrate into the plant cell genome in a site-specific manner, whereupon it can be operatively linked to an endogenous nucleotide sequence, which can be expressed in response to a stress condition specific for the regulatory element; or can be a mutant regulatory element, which is not responsive to the stress condition, whereby upon integrating into the plant cell genome, the mutant regulatory element disrupts an endogenous stress-regulated regulatory element of a plant stress-regulated gene, thereby altering the responsiveness of the plant stress-regulated gene to the stress condition. Accordingly, the invention also provides genetically modified plants, including transgenic plants, produced by such a method, and a plant cell

obtained from such genetically modified plant, wherein said plant cell exhibits altered responsiveness to the stress condition; a seed produced by a transgenic plant; and a cDNA library prepared from a transgenic plant.

[0159] Also provided is a method of modulating the responsiveness of a plant cell to a stress condition. Such a method can be performed, for example, by introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, thereby modulating the responsiveness of the plant cell to a stress condition. As disclosed herein, the responsiveness of the plant cell can be increased or decreased upon exposure to the stress condition, and the altered responsiveness can result in increased or decreased tolerance of the plant cell to a stress condition. The polynucleotide portion of the plant stress-regulated gene can, but need not, be integrated into the genome of the plant cell, thereby modulating the responsiveness of the plant cell to the stress condition. Accordingly, the invention also provide a genetically modified plant, including a transgenic plant, which contains an introduced polynucleotide portion of a plant stress-regulated gene, as well as plant cells, tissues, and the like, which exhibit modulated responsiveness to a stress condition.

[0160] The polynucleotide portion of the plant stress-regulated gene can encode a stress-regulated polypeptide or functional peptide portion thereof, which can be operatively linked to a heterologous promoter. As used herein, reference to a "functional peptide portion of a plant stress-regulated polypeptide" means a contiguous amino acid sequence of the polypeptide that has an activity of the full length polypeptide, or that has an antagonist activity with respect to the full length polypeptide, or that presents an epitope unique to the polypeptide. Thus, by expressing a functional peptide portion of a plant stress-regulated polypeptide in a plant cell, the peptide can act as an agonist or an antagonist of the polypeptide, thereby modulating the responsiveness of the plant cell to a stress condition.

[0161] A polynucleotide portion of the plant stress-regulated nucleotide sequence also can contain a mutation, whereby upon integrating into the plant cell genome, the

polynucleotide disrupts (knocks-out) an endogenous plant stress-regulated nucleotide sequence, thereby modulating the responsiveness of said plant cell to the stress condition. Depending on whether the knocked-out gene encodes an adaptive or a maladaptive stress-regulated polypeptide, the responsiveness of the plant will be modulated accordingly. Thus, a method of the invention provides a means of producing a transgenic plant having a knock-out phenotype of a plant stress-regulated nucleotide sequence.

[0162] Alternatively, the responsiveness of a plant or plant cell to a stress condition can be modulated by use of a suppressor construct containing dominant negative mutation for any of the stress-regulated sequences described herein. Expression of a suppressor construct containing a dominant mutant mutation generates a mutant transcript that, when coexpressed with the wild-type transcript inhibits the action of the wild-type transcript. Methods for the design and use of dominant negative constructs are well known (see, for example, in Herskowitz, Nature 329:219-222, 1987; Lagna and Hemmati-Brivanlou, Curr. Topics Devel. Biol. 36:75-98, 1998).

[0163] The polynucleotide portion of the plant stress-regulated gene also can comprise a stress-regulated regulatory element, which can be operatively linked to a heterologous nucleotide sequence, which, upon expression from the regulatory element in response to a stress condition, modulates the responsiveness of the plant cell to the stress condition. Such a heterologous nucleotide sequence can encode, for example, a stress-inducible transcription factor such as DREB1A, which, upon exposure to the stress condition, is expressed such that it can amplify the stress response (see Kasuga et al., *supra*, 1999). The heterologous nucleotide sequence also can encode a polynucleotide that is specific for a plant stress-regulated gene, for example, an antisense molecule, a ribozyme, and a triplexing agent, either of which, upon expression in the plant cell, reduces or inhibits expression of a stress-regulated polypeptide encoded by the gene, thereby modulating the responsiveness of the plant cell to a stress condition, for example, an abnormal level of cold, osmotic pressure,

and salinity. As used herein, the term "abnormal," when used in reference to a condition such as temperature, osmotic pressure, salinity, or any other condition that can be a stress condition, means that the condition varies sufficiently from a range generally considered optimum for growth of a plant that the condition results in an induction of a stress response in a plant. Methods of determining whether a stress response has been induced in a plant are disclosed herein or otherwise known in the art.

[0164] A plant stress-regulated regulatory element can be operatively linked to a heterologous polynucleotide sequence, such that the regulatory element can be introduced into a plant genome in a site-specific matter by homologous recombination. For example, a mutant plant stress-regulated regulatory element for a maladaptive stress-induced polypeptide can be transformed into a plant genome in a site specific manner by *in vivo* mutagenesis, using a hybrid RNA-DNA oligonucleotide ("chimeroplast" (TIBTECH 15:441- 447, 1997; W0 95/15972; Kren, Hepatology 25:1462-1468, 1997; Cole-Strauss, Science 273:1386-1389, 1996, each of which is incorporated herein by reference). Part of the DNA component of the RNA-DNA oligonucleotide is homologous to a nucleotide sequence comprising the regulatory element of the maladaptive gene, but includes a mutation or contains a heterologous region which is surrounded by the homologous regions. By means of base pairing of the homologous regions of the RNA-DNA oligonucleotide and of the endogenous nucleic acid molecule, followed by a homologous recombination the mutation contained in the DNA component of the RNA-DNA oligonucleotide or the heterologous region can be transferred to the plant genome, resulting in a "mutant" gene that, for example, is not induced in response to a stress and, therefore, does not confer the maladaptive phenotype. Such a method similarly can be used to knock-out the activity of a stress-regulated gene, for example, in an undesirable plant. Such a method can provide the advantage that a desirable wild-type plant need not compete with the undesirable plant, for example, for light, nutrients, or the like.

[0165] A method of modulating the responsiveness of a plant cell to a stress condition also can be performed by introducing a mutation in the chromosomal copy of a plant stress-regulated gene, for example, in the stress-regulated regulatory element, by transforming a cell with a chimeric oligonucleotide composed of a contiguous stretch of RNA and DNA residues in a duplex conformation with double hairpin caps on the ends. An additional feature of the oligonucleotide is the presence of 2'-0- methylation at the RNA residues. The RNA/DNA sequence is designed to align with the sequence of a chromosomal copy of the target regulatory element and to contain the desired nucleotide change (see U.S. Pat. No. 5,501,967, which is incorporated herein by reference).

[0166] A plant stress-regulated regulatory element also can be operatively linked to a heterologous polynucleotide such that, upon expression from the regulatory element in the plant cell, confers a desirable phenotype on the plant cell. For example, the heterologous polynucleotide can encode an aptamer, which can bind to a stress-induced polypeptide. Aptamers are nucleic acid molecules that are selected based on their ability to bind to and inhibit the activity of a protein or metabolite. Aptamers can be obtained by the SELEX (Systematic Evolution of Ligands by Exponential Enrichment) method (see U.S. Pat. No. 5,270,163), wherein a candidate mixture of single stranded nucleic acids having regions of randomized sequence is contacted with a target, and those nucleic acids having a specific affinity to the target are partitioned from the remainder of the candidate mixture, and amplified to yield a ligand enriched mixture. After several iterations a nucleic acid molecule (aptamer) having optimal affinity for the target is obtained. For example, such a nucleic acid molecule can be operatively linked to a plant stress-regulated regulatory element and introduced into a plant. Where the aptamer is selected for binding to a polypeptide that normally is expressed from the regulatory element and is involved in an adaptive response of the plant to a stress, the recombinant molecule comprising the aptamer can be useful for inhibiting the activity of the stress-regulated polypeptide, thereby decreasing the tolerance of the plant to the stress condition.

[0167] The invention provides a genetically modified plant, which can be a transgenic plant, that is tolerant or resistant to a stress condition. As used herein, the term "tolerant" or "resistant," when used in reference to a stress condition of a plant, means that the particular plant, when exposed to a stress condition, shows less of an effect, or no effect, in response to the condition as compared to a corresponding reference plant (naturally occurring wild-type plant or a plant not containing a construct of the present invention). As a consequence, a plant encompassed within the present invention grows better under more widely varying conditions, has higher yields and/or produces more seeds. Thus, a transgenic plant produced according to a method of the invention can demonstrate protection (as compared to a corresponding reference plant) from a delay to complete inhibition of alteration in cellular metabolism, or reduced cell growth or cell death caused by the stress. Preferably, the transgenic plant is capable of substantially normal growth under environmental conditions where the corresponding reference plant shows reduced growth, metabolism or viability, or increased male or female sterility.

[0168] The determination that a plant modified according to a method of the invention has increased resistance to a stress-inducing condition can be made by comparing the treated plant with a control (reference) plant using well known methods. For example, a plant having increased tolerance to saline stress can be identified by growing the plant on a medium such as soil, which contains a higher content of salt in the order of at least about 10% compared to a medium the corresponding reference plant is capable of growing on. Advantageously, a plant treated according to a method of the invention can grow on a medium or soil containing at least about 50%, or more than about 75%, particularly at least about more than 100%, and preferably more than about 200% salt than the medium or soil on which a corresponding reference plant can grow. In particular, such a treated plant can grow on medium or soil containing at least 40 mM, generally at least 100 mM, particularly at least 200 mM, and preferably at least 300 mM salt, including, for example, a water soluble inorganic salt such as sodium sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium

chloride, or the like; salts of agricultural fertilizers, and salts associated with alkaline or acid soil conditions; particularly NaCl.

[0169] In another embodiment, the invention provides a plant that is less tolerant or less resistant to a stress condition as compared to a corresponding reference plant. As used herein, the term "less tolerant" or "less resistant," when used in reference to a stress condition of a plant, means that the particular plant, when exposed to a stress condition, shows an alteration in response to the condition as compared to a corresponding reference plant. As a consequence, such a plant, which generally is an undesirable plant species, is less likely to grow when exposed to a stress condition than an untreated plant.

[0170] The present invention also relates to a method of expressing a heterologous nucleotide sequence in a plant cell. Such a method can be performed, for example, by introducing into the plant cell a plant stress-regulated regulatory element operatively linked to the heterologous nucleotide sequence, whereby, upon exposure of the plant cell to stress condition, the heterologous nucleotide sequence is expressed in the plant cell. The heterologous nucleotide sequence can encode a selectable marker, or preferably, a polypeptide that confers a desirable trait upon the plant cell, for example, a polypeptide that improves the nutritional value, digestibility or ornamental value of the plant cell, or a plant comprising the plant cell. Accordingly, the invention provides a transgenic plant that, in response to a stress condition, can produce a heterologous polypeptide from a plant stress-regulated regulatory element. Such transgenic plants can provide the advantage that, when grown in a cold environment for example, expression of the heterologous polypeptide from a plant cold-regulated regulatory element can result in increased nutritional value of the plant.

[0171] The present invention further relates to a method of modulating the activity of a biological pathway in a plant cell, wherein the pathway involves a stress-regulated polypeptide. As used herein, reference to a pathway that "involves" a stress-regulated polypeptide means that the polypeptide is required for normal

function of the pathway. For example, plant stress-regulated polypeptides as disclosed herein include those acting as kinases or as transcription factors, which are well known to be involved in signal transduction pathways. As such, a method of the invention provides a means to modulate biological pathways involving plant stress-regulated polypeptides, for example, by altering the expression of the polypeptides in response to a stress condition. Thus, a method of the invention can be performed, for example, by introducing a polynucleotide portion of a plant stress-regulated gene into the plant cell, thereby modulating the activity of the biological pathway.

[0172] A method of the invention can be performed with respect to a pathway involving any of the stress-regulated polypeptides as encoded by a polynucleotide of SEQ ID NOS:1-2703, including for example, a stress-regulated transcription factor, an enzyme, including a kinase, a channel protein (see, for example, Tables 29-31; see, also, Table 1). Pathways in which the disclosed stress-regulated stress factors are involved can be identified, for example, by searching the Munich Information Center for Protein Sequences (MIPS) *Arabidopsis thaliana* database (MATDB), which is at http://www.mips.biochem.mpg.de/proj/thal/.

[0173] The present invention also relates to a method of identifying a polynucleotide that modulates a stress response in a plant cell. Such a method can be performed, for example, by contacting an array of probes representative of a plant cell genome and nucleic acid molecules expressed in plant cell exposed to the stress; detecting a nucleic acid molecule that is expressed at a level different from a level of expression in the absence of the stress; introducing the nucleic acid molecule that is expressed differently into a plant cell; and detecting a modulated response of the plant cell containing the introduced nucleic acid molecule to a stress, thereby identifying a polynucleotide that modulates a stress response in a plant cell. The contacting is under conditions that allow for selective hybridization of a nucleic acid molecule with probe having sufficient complementarity, for example, under stringent hybridization conditions.

[0174] As used herein, the term "array of probes representative of a plant cell genome" means an organized group of oligonucleotide probes that are linked to a solid support, for example, a microchip or a glass slide, wherein the probes can hybridize specifically and selectively to nucleic acid molecules expressed in a plant cell. Such an array is exemplified herein by a GeneChip® Arabidopsis Genome Array (Affymetrix; see Example 1). In general, an array of probes that is "representative" of a plant genome will identify at least about 30% or the expressed nucleic acid molecules in a plant cell, generally at least about 50% or 70%, particularly at least about 80% or 90%, and preferably will identify all of the expressed nucleic acid molecules. It should be recognized that the greater the representation, the more likely all nucleotide sequences of cluster of stress-regulated genes will be identified.

[0175] A method of the invention is exemplified in Example 1, wherein clusters of *Arabidopsis* genes induced to cold, to increased salinity, to increased osmotic pressure, and to a combination of the above three stress conditions were identified. Based on the present disclosure, the artisan readily can obtain nucleic acid samples for *Arabidopsis* plants exposed to other stress conditions, or combinations of stress conditions, and identify clusters of genes induced in response to the stress conditions. Similarly, the method is readily adaptable to identifying clusters of stress-regulated genes expressed in other plant species, particularly commercially valuable plant species, where a substantial amount of information is known regarding the genome.

[0176] The clusters of genes identified herein include those clusters of genes that are induced or repressed in response to a combination of stress conditions, but not to any of the stress conditions alone; and clusters of genes that are induced or repressed in response to a selected stress condition, but not to other stress conditions tested. Furthermore, clusters of genes that respond to a stress condition in a temporally regulated manner are also included, such as gene clusters that are induced early (for example, within about 3 hours), late (for example, after about 8 to 24 hours), or continuously in a stress response. In addition, the genes within a cluster are represented by a variety of cellular proteins, including transcription factors, enzymes

such as kinases, channel proteins, and the like (see Tables 1 and 29-31). Thus, the present invention further characterizes nucleotide sequences that previously were known to encode cellular peptides by classifying them within clusters of stress-regulated genes.

[0177] The present invention additionally relates to a method of identifying a stress condition to which a plant cell was exposed. Such a method can be performed, for example, by contacting nucleic acid molecules expressed in the plant cell and an array of probes representative of the plant cell genome; and detecting a profile of expressed nucleic acid molecules characteristic of a stress response, thereby identifying the stress condition to which the plant cell was exposed. The contacting generally is under conditions that allow for selective hybridization of a nucleic acid molecule with probe having sufficient complementarity, for example, under stringent hybridization conditions. The profile can be characteristic of exposure to a single stress condition, for example, an abnormal level of cold, osmotic pressure, or salinity (Tables 3-14), or can be characteristic of exposure to more than one stress condition (Tables 15-26, for example, cold, increased osmotic pressure and increased salinity (see Tables 24-26).

[0178] The method can be practiced using at least one nucleic acid probe and can identify one or combination of stress conditions by detecting altered expression of one or a plurality of polynucleotides representative of plant stress-regulated genes. As used herein, the term "at least one" includes one, two, three or more, for example, five, ten, twenty, fifty or more polynucleotides, nucleic acid probes, and the like. The term "plurality" is used herein to mean two or more, for example, three, four, five or more, including ten, twenty, fifty or more polynucleotides, nucleic acid probes, and the like.

[0179] In a method of the invention, nucleic acid samples from the plant cells to be collected can be contacted with an array, then the profile can be compared with known expression profiles prepared from nucleic acid samples of plants exposed to a

known stress condition or combination of stress conditions. By creating a panel of such profiles, representative of various stress conditions, an unknown stress condition to which a plant was exposed can be identified simply by comparing the unknown profile with the known profiles and determining which known profile that matches the unknown profile. Preferably, the comparison is automated. Such a method can be useful, for example, to identify a cause of damage to a crop, where the condition causing the stress is not known or gradually increases over time. For example, accumulation in soils over time of salts from irrigation water can result in gradually decreasing crop yields. Because the accumulation is gradual, the cause of the decreased yield may not be readily apparent. Using the present methods, it is possible to evaluate the stress to which the plants are exposed, thus revealing the cause of the decreased yields.

[0180] The present invention, therefore includes a computer readable medium containing executable instructions form receiving expression data for sequences substantially similar to any of those disclosed herein and comparing expression data from a test plant to a reference plant that has been exposed to an abiotic stress. Also provided is a computer-readable medium containing sequence data for sequences substantially similar to any of the sequences described herein, or the complements thereof, and a module for comparing such sequences to other nucleic acid sequences.

[0181] Also provided are plants and plant cells comprising plant stress-regulatory elements of the present invention operably linked to a nucleotide sequence encoding a detectable signal. Such plants can be used as diagnostic or "sentinel" plants to provide early warning that nearby plants are being stressed so that appropriate actions can be taken. In one embodiment, the signal is one that alters the appearance of the plant. For example, an osmotic stress regulatory element of the present invention can be operably linked to a nucleotide sequence encoding a fluorescent protein such as green fluorescent protein. When subjected to osmotic stress, the expression of the green fluorescent protein in the sentinel plant provides a visible signal so that appropriate actions can be taken to remove or alleviate the stress. The use of

fluorescent proteins in plants is well known (see, for example, in Leffel et al., BioTechniques 23:912, 1997).

[0182] The invention further relates to a method of identifying an agent that modulates the activity of a stress-regulated regulatory element of a plant. As used herein, the term "modulate the activity," when used in reference to a plant stress-regulated regulatory element, means that expression of a polynucleotide from the regulatory element is increased or decreased. In particular, expression can be increased or decreased with respect to the basal activity of the promoter, i.e., the level of expression, if any, in the absence of a stress condition that normally induces expression from the regulatory element; or can be increased or decreased with respect to the level of expression in the presence of the inducing stress condition. As such, an agent can act as a mimic of a stress condition, or can act to modulate the response to a stress condition.

[0183] Such a method can be performed, for example, by contacting the regulatory element with an agent suspected of having the ability to modulate the activity of the regulatory element, and detecting a change in the activity of the regulatory element. In one embodiment, the regulatory element can be operatively linked to a heterologous polynucleotide encoding a reporter molecule, and an agent that modulates the activity of the stress-regulated regulatory element can be identified by detecting a change in expression of the reporter molecule due to contacting the regulatory element with the agent. Such a method can be performed *in vitro* in a plant cell-free system, or in a plant cell in culture or in a plant *in situ*.

[0184] A method of the invention also can be performed by contacting the agent is contacted with a genetically modified cell or a transgenic plant containing an introduced plant stress-regulated regulatory element, and an agent that modulates the activity of the regulatory element is identified by detecting a phenotypic change in the modified cell or transgenic plant.

[0185] A method of the invention can be performed in the presence or absence of the stress condition to which the particularly regulatory element is responsive. As such, the method can identify an agent that modulates the activity of plant stress-regulated promoter in response to the stress, for example, an agent that can enhance the stress response or can reduce the stress response. In particular, a method of the invention can identify an agent that selectively activates the stress-regulated regulatory elements of a cluster of plant stress-regulated genes, but does not affect the activity of other stress-regulated regulatory genes. As such, the method provides a means to identify an agent that acts as a stress mimic. Such agents can be particularly useful to prepare a plant to an expected stress condition. For example, a agent that acts as a cold mimic can be applied to a field of plants prior to the arrival of an expected cold front. Thus, the cold stress response can be induced prior to the actual cold weather, thereby providing the plants with the protection of the stress response, without the plants suffering from any initial damage due to the cold. Similarly, an osmotic pressure mimic can be applied to a crop of plants prior a field being flooded by a rising river.

[0186] In one embodiment, the present invention provides a method for marker-assisted selection. Marker-assisted selection involves the selection of plants having desirable phenotypes based on the presence of particular nucleotide sequences ("markers"). The use of markers allows plants to be selected early in development, often before the phenotype would normally be manifest. Because it allows for early selection, marker-assisted selection decreases the amount of time need for selection and thus allows more rapid genetic progress.

[0187] Briefly, marker-assisted selection involves obtaining nucleic acid from a plant to be selected. The nucleic acid obtained is then probed with probes that selectively hybridize under stringent, preferably highly stringent, conditions to a nucleotide sequence or sequences associated with the desired phenotype. In one embodiment, the probes hybridize to any of the stress-responsive genes or regulatory regions disclosed herein, for example, any one of SEQ ID NOS:1-2703. The presence

of any hybridization products formed is detected and plants are then selected on the presence or absence of the hybridization products.

[0188] The following examples are intended to illustrate but not limit the invention.

EXAMPLE 1

PROFILING OF PLANT STRESS-REGULATED GENES

[0189] This example demonstrates that clusters of stress-regulated genes can be identified in plant cells exposed to various stress conditions, either alone or in combination.

[0190] A GeneChip® Arabidopsis Genome Array (Affymetrix, Santa Clara, CA) was used to identify clusters of genes that were coordinately induced in response to various stress conditions. The GeneChip® Arabidopsis Genome Array contains probes synthesized *in situ* and is designed to measure temporal and spatial gene expression of approximately 8700 genes in greater than 100 EST clusters. The sequences used to develop the array were obtained from GenBank (http://www.ncbi.nlm.nih.gov/) in collaboration with Torrey Mesa Research Institute (San Diego, CA), formerly known as Novartis Agriculture Discovery Institute. Eighty percent of the nucleotide sequences represented on the array are predicted coding sequences from genomic BAC entries; twenty percent are high quality cDNA sequences. The array also contains over 100 EST clusters that share homology with the predicted coding sequences from BAC clones (see, for example, world wide web at address (url) "affymetrix.com/products/Arabidopsis_content.html".

[0191] The Affymetrix GeneChip® array was used to define nucleotide sequences/ pathways affected by various abiotic stresses and to define which are uniquely regulated by one stress and those that respond to multiple stress, and to identify candidate nucleotide sequences for screening for insertional mutants. Of the approximately 8,700 nucleotide sequences represented on the Affymetrix GeneChip® array, 2862 nucleotide sequences showed at least a 2-fold change in expression in at

least one sample, relative to no-treatment controls. Of those 2,862 nucleotide sequences 1,335 were regulated only by cold stress, 166 were regulated only mannitol stress and 209 were regulated only by saline stress. Furthermore, of the 2,862 nucleotide sequences 123 nucleotide sequences were regulated by salt and mannitol stress, 293 were regulated by mannitol and cold stress, 274 were regulated by cold and saline stress and 462 were regulated by cold, mannitol and salt. Of the 2,862 nucleotide sequences, 771 passed the higher stringency of showing at least a 2-fold change in expression in at least 2 samples, relative to control. And, 508 of the 771 nucleotide sequences were found in an in-house collection of insertion mutants.

[0192] The following describes in more detail how the experiments were done. Transcriptional profiling was performed by hybridizing fluorescence labeled cRNA with the oligonucleotides probes on the chip, washing, and scanning. Each gene is represented on the chip by about sixteen oligonucleotides (25-mers). Expression level is related to fluorescence intensity. Starting material contained 1 to 10 μg total RNA; detection specificity was about $1:10^6$; approximately a 2-fold change was detectable, with less than 2% false positive; the dynamic range was approximately 500x. Nucleotide sequences having up to 70% to 80% identity could be discriminated using this system.

[0193] Seven day old axenic *Arabidopsis* seedlings were transferred to Magenta boxes with rafts floating on MS medium. Three weeks later (28 day old seedlings), stresses were applied as follows: Control - no treatment; Cold - Magenta box placed in ice; Mannitol - medium + 200 mM mannitol; Salt - medium + 100 mM NaCl. Tissue samples were collected at 3 hours and 27 hours into the stress, roots and aerial portions were harvested, RNA was purified, and the samples were analyzed using the GeneChip® Arabidopsis Genome Array (Affymetrix, Santa Clara, CA) following the manufacturer's protocol.

[0194] Raw fluorescence values as generated by Affymetrix software were processed as follows: the values were brought into Microsoft Excel and values of

25 or less were set to 25 (an empirically determined baseline, Zhu and Wang, Plant Physiol. 124:1472-1476; 2000). The values from the stressed samples were then converted to fold change relative to control by dividing the values from the stressed samples by the values from the no-treatment control samples. Expression patterns that were altered at least 2-fold with respect to the control were selected. This method gave very robust results and resulted in a larger number of nucleotide sequences called as stress-regulated than previous methods had permitted.

[0195] Based on the profiles obtained following hybridization of nucleic acid molecules obtained from plant cells exposed to various stress conditions to the probes in the microarray, clusters of nucleotide sequences that were altered in response to the stress conditions were identified (see Tables 3-6, cold responsive; Tables 7-10, salt (saline) responsive; Tables 11 to 14, mannitol (osmotic) responsive; Tables 15-17, cold and mannitol responsive; Tables 18-20, 6 salt and cold responsive; Tables 21-23, salt and mannitol responsive; Tables 24-26, cold, salt and mannitol responsive. Examples of plant gene sequences that varied in expression at least two-fold in response to a combination of cold, saline and osmotic stress in root cells and leaf cells are shown in Tables 27 and 28, respectively. In addition, examples of plant gene sequences that encode transcription factors (Table 29), phosphatases (Table 30), and kinases (Table 31) and that varied at least two-fold in response to a combination of cold, saline and osmotic stress are provided.

[0196] Affymetrix ID numbers and corresponding SEQ ID NOS: for the respective *Arabidopsis* nucleotide sequences are provided Tables 3-26, and can be used to determine SEQ ID NOS: for the sequences shown by Affymetrix ID number in Tables 27-31. The Affymetrix ID number refers to a particular nucleotide sequence on the GeneChip® Arabidopsis Genome Array. In some cases, a particular plant stress-regulated gene sequence hybridized to more than one nucleotide sequence on the GeneChip® Arabidopsis Genome Array (see, for example, Table 3, where SEQ ID NO:36 is shown to have hybridized to the 12187_AT and 15920_I_AT nucleotide sequences on the GeneChip®). In addition, it should be recognized that the disclosed

sequences are not limited to coding sequences but, in some cases, include 5' untranslated sequences (see Table 2) or a longest coding region. As such, while the sequences set forth as SEQ ID NOS:1-2073 generally start with an ATG codon, in most cases each comprises a longer nucleotide sequence, including a regulatory region (see Table 2).

[0197] The results disclosed herein demonstrate that several polynucleotides, some of which were known to function as transcription factors, enzymes, and structural proteins, also are involved in the response of a plant cell to stress. The identification of the clusters of stress-regulated genes as disclosed herein provides a means to identify stress-regulated regulatory elements present in *Arabidopsis thaliana* nucleotide sequences, including consensus regulatory elements. It should be recognized, however that the regulatory elements of the plant genes comprising a sequence as set forth in SEQ ID NOS:156, 229, 233, 558, 573, 606, 625, 635, 787, and 813, which previously have been described as cold regulated genes, are not encompassed within the stress-regulated gene regulatory element of the invention, and the regulatory elements of the plant genes comprising the nucleotide sequences set forth as SEQ ID NOS:1263, 1386, 1391, 1405, 1445, 1484, 1589, 1609, 1634, 1726, 1866, 1918, and 1928, which previously have been identified as genes that are responsive to a single stress condition such as cold or saline stress, are not encompassed within the plant stress-regulated gene regulatory elements of the invention to the extent that they confer stress-regulated expression only with respect to the known single stress. Furthermore, the identification of the *Arabidopsis* stress-regulated genes provides a means to identify the corresponding homologs and orthologs in other plants, including commercially valuable food crops such as wheat, rice, soy, and barley, and ornamental plants. BLASTN and BLASTP searches to identify such sequences revealed the polynucleotide sequences set forth in Table 32, which is on the CD-R compact disc submitted herewith.

[0198] Although the invention has been described with reference to the above example, it will be understood that modifications and variations are encompassed within the spirit and scope of the invention. Accordingly, the invention is limited only by the claims, which follow Tables 1 to 31.

TABLE 1

SEQUENCE DESCRIPTIONS

Seq ID	Description
1	unknown protein
2	unknown protein
3	unknown protein
4	putative auxin-induced protein
5	unknown protein
6	hypothetical protein
7	putative protein
8	unknown protein
9	unknown protein
10	unknown protein
11	putative protein
12	Thioredoxin - like protein
13	putative RNA helicase
14	putative protein
15	putative protein
16	RING zinc finger protein, putative
17	putative cyclin
18	putative protein
19	putative protein
20	unknown protein
21	putative protein
22	putative protein
23	hypothetical protein
24	unknown protein
25	hypothetical protein
26	unknown protein
27	unknown protein
28	unknown protein
29	unknown protein
30	putative protein
31	putative protein
32	putative protein
33	unknown protein
34	putative ribonuclease III
35	unknown protein
36	unknown protein
37	unknown protein
38	unknown protein
39	unknown protein
40	putative histidine kinase
41	scarecrow-like 7 (SCL7)
42	putative protein
43	No function assigned by TIGR
44	unknown protein
45	unknown protein

SEQ ID	Description
46	succinyl-CoA-ligase alpha subunit
47	putative protein
48	CLV1 receptor kinase like protein
49	putative receptor-like protein kinase
50	putative squalene synthase
51	putative receptor protein kinase
52	somatic embryogenesis receptor-like kinase, putative
53	putative protein
54	putative beta-glucosidase
55	multi-drug resistance protein
56	receptor protein kinase (TMK1), putative
57	putative receptor-like protein kinase
58	putative pectate lyase
59	putative protein kinase
60	putative peroxidase
61	cytochrome P450-like protein
62	putative beta-amylase
63	monosaccharide transporter STP3
64	Lycopersicon esculentum proteinase TMP, Pir2:T07617
65	putative receptor-like protein kinase
66	G-box-binding factor 1
67	amino acid carrier, putative
68	myb-related protein
69	No function assigned by TIGR
70	SNF1 like protein kinase
71	Cu/Zn superoxide dismutase-like protein
72	putative protein kinase
73	small nuclear ribonucleoprotein U1A

TABLE 1 (cont)

74	ras-like GTP-binding protein
75	oleoyl-[acyl-carrier-protein] hydrolase-like protein
76	putative heat shock transcription factor
77	putative protein
78	membrane-bound small GTP-binding - like protein
79	putative protein (fragment)
80	indole-3-acetate beta-glucosyltransferase like protein
81	HD-zip transcription factor (athb-8)
82	putative cAMP-dependent protein kinase
83	glucuronosyl transferase-like protein
84	putative leucine-rich repeat disease resistance protein
85	98b like protein
86	putative receptor-like protein kinase
87	IAA-Ala hydrolase (IAR3)
88	putative AP2 domain transcription factor
89	putative expansin
90	putative Ap2 domain protein
91	expansin (At-EXP1)
92	cytochrome P450 - like protein
93	putative ATP-dependent RNA helicase A
94	unknown protein
95	predicted protein
96	putative glucosyltransferase
97	unknown protein
98	putative xyloglucan-specific glucanase
99	cysteine synthase
100	clathrin assembly protein AP19 homolog
101	dynein light chain like protein
102	chaperonin CPN10
103	putative bHLH transcription factor
104	putative glyoxysomal malate dehydrogenase precursor
105	ATP-dependent RNA helicase, putative
106	chlorophyll synthetase
107	similar to epoxide hydrolases
108	putative protein
109	unknown protein
110	hypothetical protein
111	putative membrane transporter
112	putative tyrosyl-tRNA synthetase
113	ARGININE/SERINE-RICH SPLICING FACTOR RSP31
114	putative oxidoreductase
115	unknown protein
116	linker histone protein, putative
117	hypothetical protein
118	putative protein
119	putative mitochondrial carrier protein
120	putative transcription factor
121	MYB-related protein
122	myb-related transcription factor, putative
123	unknown protein
124	unknown protein
125	putative glycine-rich protein
126	No function assigned by TIGR
127	unknown protein
128	unknown protein
129	unknown protein
130	unknown protein
131	putative membrane channel protein
132	putative protein
133	unknown protein
134	gamma glutamyl hydrolase, putative
135	40S ribosomal protein S5
136	DnaJ-like protein
137	40S ribosomal protein S26
138	putative WRKY-type DNA binding protein

TABLE 1 (cont)

139	putative protein
140	hypothetical protein
141	putative ubiquitin-conjugating enzyme
142	peptidylprolyl isomerase ROC1
143	glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)
144	No function assigned by TIGR
145	putative protein
146	putative thioredoxin
147	thioredoxin h, putative
148	thioredoxin-like
149	allene oxide synthase (emb|CAA73184.1)
150	anthranilate synthase component I-1 precursor (sp|P32068)
151	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A
152	protein kinase cdc2 homolog B
153	ethylene responsive element binding factor 1 (frameshift !)
154	ethylene responsive element binding factor 2 (ATERF2) (sp|O80338)
155	ethylene responsive element binding factor 5 (ATERF5) (sp|O80341)
156	glucose-6-phosphate dehydrogenase
157	photomorphogenesis repressor (COP1)
158	unknown protein
159	DNA (cytosine-5)-methyltransferase (DNA methyltransferase) (DNA metase) (sp|P34881)
160	PROLIFERA
161	putative photomorphogenesis repressor protein
162	SNF1-like protein kinase (AKin11)
163	thioredoxin h
164	thioredoxin
165	Ca2+-dependent lipid-binding protein, putative
166	putative auxin-induced protein
167	putative bZIP transcription factor
168	hypothetical protein
169	putative AVR9 elicitor response protein
170	putative serine/threonine protein kinase
171	bZIP transcription factor ATB2
172	putative spliceosome associated protein
173	3-hydroxyisobutyryl-coenzyme A hydrolase - like protein
174	putative protein
175	putative Mutator-like transposase
176	putative protein
177	unknown protein
178	putative protein
179	putative protein
180	putative galactinol synthase
181	putative transcriptional regulator
182	nuclear matrix constituent protein 1 (NMCP1)-like
183	putative DNA-binding protein RAV2
184	No function assigned by TIGR
185	basic blue protein, 5' partial
186	unknown protein
187	putative calcium-binding protein, calreticulin
188	putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase
189	ribosomal protein L11, cytosolic
190	putative dTDP-glucose 4-6-dehydratase
191	40S ribosomal protein S20-like protein
192	60S ribosomal protein L24

TABLE 1 (cont)

193 coatomer-like protein, epsilon subunit
194 glycoprotein(EP1), putative
195 putative SPL1-related protein
196 unknown protein
197 putative transport protein SEC61 beta-subunit
198 unknown protein
199 putative cytochrome P450
200 UTP-glucose glucosyltransferase - like protein
201 60S ribosomal protein L23
202 40S ribosomal protein S17
203 40S ribosomal protein S26
204 protein translation factor Sui1 homolog, putative
205 unknown protein
206 gamma glutamyl hydrolase, putative
207 dTDP-glucose 4,6-dehydratase, putative
208 extensin - like protein
209 unknown protein
210 protein phosphatase 2C - like protein
211 ubiquitin-like protein
212 protein phosphatase 2C-like protein
213 unknown protein
214 putative RING zinc finger ankyrin protein
215 unknown protein
216 putative rubisco subunit binding-protein alpha subunit
217 putative acetone-cyanohydrin lyase
218 putative isoamylase
219 putative protein
220 HSP associated protein like
221 60S ribosomal protein L39
222 unknown protein
223 putative SF16 protein {Helianthus annuus}
224 unknown protein
225 thioredoxin
226 trehalose-6-phosphate phosphatase (AtTPPB)
227 chlorophyll a/b-binding protein
228 class IV chitinase (CHIV)
229 chalcone synthase (naringenin-chalcone synthase) (testa 4 protein) (sp|P13114)
230 unknown protein
231 cinnamyl-alcohol dehydrogenase ELI3-2
232 farnesyl-pyrophosphate synthetase FPS2
233 phospholipid hydroperoxide glutathione peroxidase
234 heat shock transcription factor HSF4
235 heat shock protein 101
236 17.6 kDa heat shock protein (AA 1-156)
237 heat shock protein 17.6A
238 heat-shock protein
239 HY5
240 putative auxin-induced protein, IAA12
241 early auxin-induced protein, IAA19
242 auxin-inducible gene (IAA2)
243 putative protein
244 putative choline kinase
245 thymidylate kinase - like protein
246 CTP synthase like protein
247 putative protein
248 putative amidase
249 4-alpha-glucanotransferase
250 hypothetical protein
251 similar to auxin-induced protein
252 putative protein
253 putative protein
254 putative protein
255 hyuC-like protein

TABLE 1 (cont)

256 putative tetracycline transporter protein
257 similar to early nodulins
258 putative protein
259 putative peptidyl-prolyl cis-trans isomerase
260 unknown protein
261 unknown protein
262 putative endochitinase
263 putative ABC transporter
264 No function assigned by TIGR
265 CONSTANS-like B-box zinc finger protein
266 unknown protein
267 unknown protein
268 putative mitochondrial processing peptidase alpha subunit
269 putative pre-mRNA splicing factor
270 putative phosphatidylserine decarboxylase
271 unknown protein
272 unknown protein
273 unknown protein
274 putative casein kinase I
275 unknown protein
276 60S ribosomal protein L23A
277 putative mitochondrial dicarboxylate carrier protein
278 enoyl-ACP reductase (enr-A)
279 putative isoamylase
280 formamidase - like protein
281 reticuline oxidase - like protein
282 unknown protein
283 putative transketolase precursor
284 putative protein
285 unknown protein
286 unknown protein
287 unknown protein
288 putative esterase D
289 predicted protein of unknown function
290 unknown protein
291 putative indole-3-glycerol phosphate synthase
292 isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase
293 kinase associated protein phosphatase
294 putative K+ channel, beta subunit
295 KNAT1 homeobox-like protein
296 PSI type II chlorophyll a/b-binding protein, putative
297 transcription factor
298 putative WD-40 repeat protein, MSI2
299 WD-40 repeat protein (MSI3)
300 putative WD-40 repeat protein, MSI4
301 unknown protein
302 hypothetical protein
303 putative protein
304 No function assigned by TIGR
305 polyphosphoinositide binding protein, putative
306 hypothetical protein
307 unknown protein
308 chloroplast ribosomal L1 - like protein
309 cold-regulated protein cor15b precursor
310 cyanohydrin lyase like protein
311 putative replication protein A1
312 putative protein
313 possible apospory-associated like protein
314 DNA binding protein GT-1, putative
315 AT-hook DNA-binding protein (AHP1)
316 putative phospholipase
317 chloroplast FtsH protease, putative

TABLE 1 (cont)

318	enoyl-CoA hydratase like protein
319	berberine bridge enzyme - like protein
320	putative sugar transporter
321	unknown protein
322	No function assigned by TIGR
323	hypothetical protein
324	putative acidic ribosomal protein
325	putative protein
326	unknown protein
327	hypothetical protein
328	putative protein
329	dihydroxypolyprenylbenzoate methyltransferase
330	unknown protein
331	myb-related protein
332	No function assigned by TIGR
333	putative protein
334	putative disease resistance response protein
335	hypothetical protein
336	No function assigned by TIGR
337	starch branching enzyme II
338	No function assigned by TIGR
339	putative enolase (2-phospho-D-glycerate hydroylase)
340	putative protein kinase
341	HD-Zip protein, putative
342	putative protein kinase
343	phenylalanyl-trna synthetase - like protein
344	putative aconitase
345	NAM(no apical meristem) protein, putative
346	unknown protein
347	putative phosphomannomutase
348	putative farnesylated protein
349	unknown protein
350	water stress-induced protein, putative
351	unknown protein
352	unknown protein
353	PEROXISOMAL MEMBRANE PROTEIN PMP22
354	putative peroxisomal membrane carrier protein
355	putative protein
356	unknown protein
357	putative protein
358	putative protein
359	argininosuccinate synthase -like protein
360	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
361	putative JUN kinase activator protein
362	putative 60S ribosomal protein L35
363	nucleoid DNA-binding protein cnd41 - like protein
364	SigA binding protein
365	hypothetical protein
366	putative protein kinase
367	unknown protein
368	regulatory protein NPR1-like; transcription factor inhibitor I kappa B-like
369	putative protein
370	hypothetical protein
371	phosphoribosylanthranilate isomerase
372	phosphoribosylanthranilate isomerase
373	sterol glucosyltransferase, putative
374	putative gigantea protein
375	putative MYB family transcription factor
376	hypothetical protein
377	hypothetical protein
378	predicted protein
379	cytochrome P450, putative

TABLE 1 (cont)

380 putative Na+ dependent ileal bile acid transporter
381 unknown protein
382 RING-H2 finger protein RHF1a
383 putative protein
384 unknown protein
385 putative protein
386 putative auxin-regulated protein
387 hypothetical protein
388 unknown protein
389 unknown protein
390 putative protein
391 putative protein
392 unknown protein
393 histone H1
394 Argonaute (AGO1)-like protein
395 unknown protein
396 putative protein with C-terminal RING finger
397 unknown protein
398 unknown protein
399 unknown protein
400 unknown protein
401 unknown protein
402 putative copper amine oxidase
403 unknown protein
404 unknown protein
405 unknown protein
406 putative protein
407 putative protein
408 unknown protein
409 unknown protein
410 putative protein
411 putative protein
412 unknown protein
413 serine/threonine kinase - like protein
414 alcohol dehydrogenase, putative
415 anthranilate phosphoribosyltransferase, chloroplast precursor (sp|Q02166)
416 phytochrome C (sp|P14714)
417 putative phytochrome-associated protein 3
418 receptor serine/threonine kinase PR5K
419 Ran-binding protein (atranbp1a)
420 small Ras-like GTP-binding protein (gb|AAB58478.1)
421 sterol-C5-desaturase
422 tryptophan synthase beta chain 1 precursor (sp|P14671)
423 thioredoxin f2 (gb|AAD35004.1)
424 No function assigned by TIGR
425 putative WRKY DNA-binding protein
426 putative protein
427 unknown protein
428 unknown protein
429 14-3-3 protein homolog RCI1 (pir||S47969)
430 unknown protein
431 putative CCCH-type zinc finger protein
432 PINHEAD (gb|AAD40098.1); translation initiation factor
433 plasma membrane proton ATPase (PMA)
434 CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR homolog
435 membrane related protein CP5, putative
436 ABC transporter (AtMRP2)
437 putative embryo-abundant protein
438 putative anthocyanidin-3-glucoside rhamnosyltransferase
439 putative lipid transfer protein
440 unknown protein
441 unknown protein
442 galactinol synthase, putative
443 putative protein
444 putative protein
445 SCARECROW-like protein
446 unknown protein

TABLE 1 (cont)

447	unknown protein
448	unknown protein
449	unknown protein
450	asparagine--tRNA ligase
451	putative protein
452	glutamate-1-semialdehyde 2,1-aminomutase 1 precursor (GSA 1) (glutamate-1-semialdehyde aminotransferase 1) (GSA-AT 1) (sp|P42799)
453	hypothetical protein
454	putative serine protease-like protein
455	No function assigned by TIGR
456	unknown protein
457	unknown protein
458	gamma-adaptin, putative
459	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - like protein
460	carbonate dehydratase - like protein
461	putative microtubule-associated protein
462	putative ribophorin I
463	putative zinc finger protein
464	chloroplast FtsH protease, putative
465	putative protein
466	unknown protein
467	putative LEA protein
468	putative protein
469	putative protein
470	unknown protein
471	putative purple acid phosphatase
472	unknown protein
473	putative protein
474	unknown protein
475	chlorophyll binding protein, putative
476	phosphoenolpyruvate carboxylase (PPC)
477	chlorophyll a/b-binding protein - like
478	AtAGP4
479	putative cryptochrome 2 apoprotein
480	type 2 peroxiredoxin, putative
481	Atpm24.1 glutathione S transferase
482	delta tonoplast integral protein (delta-TIP)
483	20S proteasome subunit (PAA2)
484	dormancy-associated protein, putative
485	putative cytidine deaminase
486	No function assigned by TIGR
487	putative phospholipase D-gamma
488	cell elongation protein, Dwarf1
489	germin-like protein
490	hevein-like protein precursor (PR-4)
491	rac-like GTP binding protein (ARAC5)
492	phosphoprotein phosphatase, type 1 catalytic subunit
493	ubiquitin-protein ligase UBC9
494	xyloglucan endotransglycosylase-related protein XTR-7
495	cysteine synthase
496	putative villin 2
497	glutathione S-transferase
498	5-adenylylsulfate reductase
499	arginine decarboxylase
500	ATHP2, putative
501	ornithine carbamoyltransferase precursor
502	puative protein
503	putative protein
504	unknown protein
505	putative protein
506	putative protein
507	unknown protein
508	unknown protein
509	unknown protein
510	unknown protein
511	hypothetical protein

TABLE 1 (cont)

512	putative protein
513	putative DnaJ protein
514	plastocyanin
515	unknown protein
516	unknown protein
517	unknown protein
518	unknown protein
519	unknown protein
520	unknown protein
521	putative ATP-dependent RNA helicase
522	non-race specific disease resistance protein (NDR1)
523	hypothetical protein
524	putative protein
525	putative protein
526	putative protein
527	copper transport protein
528	putative protein
529	unknown protein
530	unknown protein
531	unknown protein
532	putative protein kinase
533	unknown protein
534	putative protein
535	putative protein
536	hypothetical protein
537	putative protein
538	putative AP2 domain transcription factor
539	putative nitrilase
540	putative protein
541	putative tetrahydrofolate synthase
542	heat-shock protein
543	unkown protein
544	unknown protein
545	histone H4
546	hypothetical protein
547	unknown protein
548	putative protein
549	predicted protein
550	putative dihydrolipoamide succinyltransferase
551	actin 3
552	putative CCCH-type zinc finger protein
553	MAP kinase kinase 2
554	ethylene-insensitive3-like1 (EIL1)
555	histidine transport protein (PTR2-B)
556	putative auxin-induced protein AUX2-11
557	hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II)
558	delta-8 sphingolipid desaturase
559	cellulose synthase catalytic subunit (Ath-A)
560	nitrate transporter (NTL1)
561	DNA-binding homeotic protein Athb-2
562	hypothetical protein
563	aspartate aminotransferase
564	4-coumarate:CoA ligase 1
565	pyruvate dehydrogenase E1 beta subunit, putative
566	nucleotide diphosphate kinase Ia (emb|CAB58230.1)
567	chloroplast Cpn21 protein
568	ATP dependent copper transporter
569	very-long-chain fatty acid condensing enzyme (CUT1)
570	putative purine-rich single-stranded DNA-binding protein
571	serine/threonine protein phosphatase (type 2A)
572	isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP2)
573	putative c2h2 zinc finger transcription factor
574	putative 20S proteasome beta subunit PBC2
575	nucleoside diphosphate kinase 3 (ndpk3)
576	ras-related small GTP-binding protein
577	putative 4-coumarate:CoA ligase 2

TABLE 1 (cont)

578 transcription factor HBP-1b homolog (sp|P43273)
579 biotin synthase (Bio B)
580 homeobox protein HAT22
581 putative preprotein translocase SECY protein
582 carbamoylphosphate synthetase, putative
583 putative protein kinase, ADK1
584 putative nuclear DNA-binding protein G2p
585 hypothetical protein
586 hypothetical protein
587 unknown protein
588 unknown protein
589 molybdopterin synthase (CNX2)
590 putative ribosomal protein L6
591 unknown protein
592 En/Spm-like transposon protein
593 putative protein
594 putative protein
595 unknown protein
596 hypothetical protein
597 unknown protein
598 unknown protein
599 putative lysosomal acid lipase
600 unknown protein
601 unknown protein
602 NifS-like aminotranfserase
603 actin 8
604 hypothetical protein
605 putative protein
606 heat-shock protein (At-hsc70-3)
607 putative protein disulfide isomerase precursor
608 adenosine nucleotide translocator
609 photosystem II oxygen-evolving complex protein 3 - like
610 sedoheptulose-bisphosphatase precursor
611 glutathione S-transferase (GST6)
612 geranylgeranyl reductase
613 hypothetical protein
614 hypothetical protein
615 phosphoribulokinase precursor
616 high mobility group protein (HMG1), putative
617 protease inhibitor II
618 protease inhibitor II
619 cytochrome P450 90A1 (sp|Q42569)
620 unknown protein
621 heat shock protein 90
622 tubulin beta-9 chain
623 putative ubiquitin carboxyl terminal hydrolase
624 protein kinase
625 DRE/CRT-binding protein DREB1C
626 histidyl-tRNA synthetase
627 splicing factor, putative
628 glutamyl-tRNA synthetase
629 putative RING zinc finger protein
630 phytochelatin synthase (gb|AAD41794.1)
631 putative C2H2-type zinc finger protein
632 putative ligand-gated ion channel protein
633 putative ribosomal-protein S6 kinase (ATPK6)
634 MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN
635 temperature-sensitive omega-3 fatty acid desaturase, chloroplast precursor (sp|P48622)
636 adenylosuccinate synthetase
637 putative 14-3-3 protein
638 putative cytochrome P450

TABLE 1 (cont)

639 putative two-component response regulator 3 protein
640 putative RING-H2 zinc finger protein ATL6
641 No function assigned by TIGR
642 small zinc finger-like protein
643 hypothetical protein
644 MAP kinase (ATMPK6)
645 vacuolar ATP synthase, putative
646 kinesin-like protein
647 serine/threonine-specific protein kinase NAK
648 No function assigned by TIGR
649 ACTIN 2/7 (sp|P53492)
650 phosphoglycerate kinase, putative
651 homeotic protein BEL1 homolog
652 proline iminopeptidase
653 pasticcino 1
654 serine/threonine protein kinase
655 cytochrome P450 monooxygenase (CYP71B4)
656 No function assigned by TIGR
657 putative GDSL-motif lipase/hydrolase
658 putative protein
659 unknown protein
660 hypothetical protein
661 putative glycosylation enzyme
662 No function assigned by TIGR
663 No function assigned by TIGR
664 unknown protein
665 putative ABC transporter
666 nifU-like protein
667 putative receptor-like protein kinase
668 putative disease resistance protein
669 receptor-like protein kinase - like
670 ubiquitin activating enzyme 2 (gb|AAB37569.1)
671 No function assigned by TIGR
672 putative receptor-like protein kinase
673 K+ transporter, AKT1
674 shaggy-like kinase beta
675 heat shock protein 70
676 plasma membrane intrinsic protein 1a
677 HSP90-like protein
678 histone H1, putative
679 unknown protein
680 dnaK-type molecular chaperone hsc70.1 - like
681 gamma-glutamylcysteine synthetase
682 peroxidase (ATP22a)
683 putative serine carboxypeptidase precursor
684 putative dioxygenase
685 glucose transporter
686 NOI protein, nitrate-induced
687 putative protein
688 putative protein
689 unknown protein
690 putative photosystem I reaction center subunit II precursor
691 putative protein
692 unknown protein
693 cobalamin biosynthesis protein
694 adenine nucleotide translocase
695 glutathione transferase, putative
696 putative 60S ribosomal protein L21
697 cytochrome P450 like protein
698 cytochrome b245 beta chain homolog RbohAp108, putative
699 RNA helicase, DRH1
700 putative aldolase
701 farnesyltransferase subunit A (FTA)

TABLE 1 (cont)

702	No function assigned by TIGR
703	putative putative sister-chromatide cohesion protein
704	calcium-dependent protein kinase
705	serine/threonine protein phosphatase type 2A, putative
706	40S ribosomal protein S28 (sp|P34789)
707	RNA polymerase subunit
708	DNA-damage-repair/toleration protein DRT102
709	putative C2H2-type zinc finger protein
710	putative adenosine phosphosulfate kinase
711	lipase
712	putative violaxanthin de-epoxidase precursor (U44133)
713	aromatic rich glycoprotein, putative
714	putative fumarase
715	flavonol synthase (FLS) (sp|Q96330)
716	response regulator 5, putative
717	sulfate transporter
718	putative floral homeotic protein, AGL9
719	putative ethylene-inducible protein
720	C-8,7 sterol isomerase
721	TCH4 protein (gb|AAA92363.1)
722	hypothetical protein
723	putative urease accessory protein
724	molybdopterin synthase sulphurylase (gb|AAD18050.1)
725	putative protein
726	NBD-like protein (gb|AAD20643.1)
727	AtHVA22c
728	unknown protein
729	phytoene synthase (gb|AAB65697.1)
730	protein kinase (AME2/AFC1)
731	hypothetical protein
732	cyclin-dependent protein kinase-like protein
733	photosystem II stability/assembly factor HCF136 (sp|O82660)
734	hypothetical protein
735	DNA binding-like protein
736	putative protein
737	chorismate mutase
738	putative LRR receptor protein kinase
739	putative chalcone synthase
740	putative protein kinase
741	replicase, putative
742	putative cysteine proteinase
743	60S ribosomal protein L36
744	unknown protein
745	CLC-b chloride channel protein
746	putative ribosomal protein S14
747	histone H2B like protein (emb|CAA69025.1)
748	60S ribosomal protein L2
749	60S ribosomal protein L15 homolog
750	ribosomal protein S27
751	ribosomal protein
752	60S ribosomal protein L12
753	60s ribosomal protein L34
754	putative ribosomal protein S10
755	drought-induced protein like
756	blue copper-binding protein, 15K (lamin)
757	calmodulin-like protein
758	putative protein
759	No function assigned by TIGR
760	alpha-mannosidase, putative
761	uncoupling protein (ucp/PUMP)

TABLE 1 (cont)

762 homeodomain - like protein
763 ribosomal protein S18, putative
764 similar to SOR1 from the fungus Cercospora nicotianae
765 60S ribosomal protein L13, BBC1 protein
766 50S ribosomal protein L24, chloroplast precursor
767 putative ribosomal protein
768 unknown protein
769 aspartate aminotransferase (AAT1)
770 potassium channel protein AtKC
771 unknown protein
772 peroxisomal targeting signal type 2 receptor
773 putative protein
774 Ras-related GTP-binding protein (ARA-4)
775 S-receptor kinase homolog 2 precursor
776 pathogenesis-related group 5 protein, putative
777 Nitrilase 4 (sp|P46011)
778 biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor (BCCP) (sp|Q42533)
779 photosystem I reaction centre subunit psaN precursor (PSI-N) (sp|P49107)
780 3(2),5-bisphosphate nucleotidase
781 high affinity Ca2+ antiporter
782 putative cytoskeletal protein
783 putative peroxidase
784 respiratory burst oxidase protein
785 beta-glucosidase
786 calcium-dependent protein kinase (pir||S71196)
787 phosphoinositide specific phospholipase C
788 similarity to S-domain receptor-like protein kinase, Zea mays
789 mitosis-specific cyclin 1b
790 4-coumarate:CoA ligase 3
791 transcription factor IIB (TFIIB)
792 unknown protein
793 hypothetical protein
794 hypothetical protein
795 sugar transporter like protein
796 putative trypsin inhibitor
797 unknown protein
798 putative multispanning membrane protein
799 receptor-like kinase, putative
800 putative inosine-5-monophosphate dehydrogenase
801 inosine-5'-monophosphate dehydrogenase, putative
802 amino acid permease 6 (emb|CAA65051.1)
803 NADPH-ferrihemoprotein reductase (ATR2)
804 putative WRKY-type DNA binding protein
805 putative ankyrin
806 putative hexose transporter
807 aquaporin/MIP - like protein
808 Ser/Thr protein kinase isolog
809 pectate lyase like protein
810 putative 60S ribosomal protein L17
811 putative protein
812 unknown protein
813 phenylalanine ammonia-lyase
814 putative cytochrome P450 monooxygenase
815 ARR1 protein, putative
816 putative bHLH transcription factor
817 aminomethyltransferase-like precursor protein
818 purple acid phosphatase precursor

TABLE 1 (cont)

819 AP2 domain containing protein, putative
820 ubiquitin-conjugating enzyme E2-21 kD 1 (ubiquitin-protein ligase 4) (ubiquitin carrier protein 4) (sp|P42748)
821 translation initiation factor
822 putative VAMP-associated protein
823 spermidine synthase, putative
824 putative protein
825 unknown protein
826 AtKAP alpha
827 glyceraldehyde-3-phosphate dehydrogenase, putative
828 putative poly(A) binding protein
829 alpha-tubulin, putative
830 serine/threonine-specific protein kinase ATPK64 (pir||S20918)
831 putative aspartate-tRNA ligase
832 ras-related small GTP-binding protein RAB1c
833 cycloartenol synthase
834 No function assigned by TIGR
835 cytochrome P450
836 GTPase AtRAB8
837 3-phosphoserine phosphatase
838 transcription factor CRC
839 nuclear cap-binding protein; CBP20 (gb|AAD29697.1)
840 chloroplast membrane protein (ALBINO3)
841 biotin holocarboxylase synthetase
842 expansin AtEx6
843 unknown protein
844 mercaptopyruvate sulfurtransferase, putative
845 putative thiosulfate sulfurtransferase
846 dihydrolipoamide S-acetyltransferase
847 auxin transport protein REH1, putative
848 putative auxin transport protein
849 apyrase (Atapy1)
850 root cap 1 (RCP1)
851 hypothetical protein
852 putative protein
853 predicted protein of unknown function
854 hypothetical protein
855 hypothetical protein
856 hypothetical protein
857 putative aldehyde dehydrogenase
858 putative peroxidase
859 UDP-glucose 4-epimerase - like protein
860 indole-3-acetate beta-glucosyltransferase like protein
861 putative beta-1,3-glucanase
862 disease resistance protein-like
863 putative respiratory burst oxidase protein B
864 ubiquitin-conjugating enzyme UBC3
865 cytoplasmic aconitate hydratase
866 NADPH oxidoreductase, putative
867 PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT -like
868 putative protein
869 unknown protein
870 60S acidic ribosomal protein P2
871 No function assigned by TIGR
872 1,4-alpha-glucan branching enzyme protein soform SBE2.2 precursor
873 calcium binding protein (CaBP-22)
874 putative phosphoglucomutase

TABLE 1 (cont)

875 shaggy-like protein kinase etha (EC 2.7.1.-)
876 pyruvate decarboxylase (gb|AAB16855.1)
877 hypothetical protein
878 putative protein kinase
879 putative protein kinase
880 putative leucine aminopeptidase
881 probable cytochrome P450
882 protein kinase 6-like protein
883 arginine methyltransferase (pam1)
884 MYB96 transcription factor-like protein
885 putative protein
886 metal ion transporter
887 No function assigned by TIGR
888 flax rust resistance protein, putative
889 fructose-2,6-bisphosphatase, putative
890 exonuclease RRP41
891 squamosa promoter binding protein-like 2 (emb|CAB56576.1)
892 putative squamosa-promoter binding protein
893 O-acetylserine(thiol) lyase, putative
894 snoRNA
895 snoRNA
896 ferredoxin-NADP+ reductase
897 H+-transporting ATP synthase chain 9 - like protein
898 photosystem I subunit III precursor, putative
899 photosystem I subunit VI precursor
900 auxin-binding protein 1 precursor
901 putative RAS superfamily GTP-binding protein
902 disease resistance protein-like
903 protein kinase like protein
904 glucuronosyl transferase-like protein
905 putative homeodomain transcription factor
906 putative flavonol reductase
907 putative protein
908 salt-tolerance protein
909 40S ribosomal protein S30
910 putative bZIP transcription factor
911 putative protein
912 putative cinnamoyl CoA reductase
913 unknown protein
914 putative RNA-binding protein
915 phosphatidylinositol synthase (PIS1)
916 unknown protein
917 hydroxyproline-rich glycoprotein homolog
918 50S ribosomal protein L15, chloroplast precursor
919 unknown protein
920 putative YME1 ATP-dependant protease
921 unknown protein
922 putative ribosomal protein L28
923 unknown protein
924 putative protein
925 protein ch-42 precursor, chloroplast
926 protein serine/threonine kinase, putative
927 beta-VPE
928 putative vacuolar sorting receptor
929 putative translation initiation factor IF-2
930 predicted protein of unknown function
931 putative protein
932 hypothetical protein
933 hypothetical protein
934 phosphate transporter, putative

TABLE 1 (cont)

935	No function assigned by TIGR
936	beta subunit of protein farnesyl transferase ERA1
937	putative glutamate decarboxylase
938	putative indole-3-acetate beta-glucosyltransferase
939	putative receptor-like protein kinase
940	UDP-galactose 4-epimerase-like protein
941	putative proliferating cell nuclear antigen, PCNA
942	ubiquitin conjugating enzyme E2 (UBC13)
943	cyclophilin (CYP2)
944	cystatin (emb|CAA03929.1)
945	putative alcohol dehydrogenase
946	acidic ribosomal protein p1
947	glutathione transferase AtGST 10 (emb|CAA10457.1)
948	putative tropinone reductase
949	ZIP4, a putative zinc transporter
950	unknown protein
951	putative protein
952	putative protein
953	putative C2H2-type zinc finger protein
954	putative RING zinc finger protein
955	putative microtubule-associated protein
956	unknown protein
957	putative protein
958	putative protein phosphatase-2c
959	V-ATPase subunit G (vag2 gene)
960	hypothetical protein
961	unknown protein
962	unknown protein
963	unknown protein
964	myrosinase-associated protein, putative
965	hypothetical protein
966	hypothetical protein
967	No function assigned by TIGR
968	unknown protein
969	hypothetical protein
970	LAX1 / AUX1 -like permease
971	putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase
972	chorismate mutase CM2
973	inner mitochondrial membrane protein
974	DEF (CLA1) protein
975	decoy
976	citrate synthase
977	myosin
978	40S ribosomal protein S19
979	ripening-related protein - like
980	putative signal peptidase I
981	methionyl-tRNA synthetase (AtcpMetRS)
982	ribosomal protein precursor - like
983	50S ribosomal protein L21 chloroplast precursor (CL21)
984	putative MYB family transcription factor
985	cyclophilin - like protein
986	hypothetical protein
987	naringenin 3-dioxygenase like protein
988	WD-repeat protein -like protein
989	putative serine carboxypeptidase II
990	prenyltransferase, putative
991	putative ligand-gated ion channel protein
992	clathrin adaptor medium chain protein MU1B, putative
993	No function assigned by TIGR

TABLE 1 (cont)

994 putative Ta11-like non-LTR retroelement protein
995 putative 3-isopropylmalate dehydrogenase
996 3-isopropylmalate dehydratase, small subunit
997 unknown protein
998 unknown protein
999 unknown protein
1000 hypothetical protein
1001 putative protein
1002 No function assigned by TIGR
1003 putative beta-glucosidase
1004 putative pectate lyase A11
1005 putative beta-glucosidase
1006 HD-Zip protein
1007 putative ubiquitin conjugating enzyme
1008 homeobox-leucine zipper protein-like
1009 cytochrome P450 like protein
1010 putative cysteine proteinase inhibitor B (cystatin B)
1011 ethylene response sensor (ERS)
1012 putative SWH1 protein
1013 putative glutathione S-transferase
1014 putative protein
1015 unknown protein
1016 putative protein phosphatase 2C
1017 dnaJ protein homolog atj3
1018 ferredoxin
1019 hypothetical protein
1020 putative sugar transport protein, ERD6
1021 putative DnaJ protein
1022 putative AP2 domain transcription factor
1023 putative protein
1024 putative cyclin-dependent kinase regulatory subunit
1025 putative tropinone reductase
1026 signal response protein (GAI)
1027 putative steroid sulfotransferase
1028 hypothetical protein
1029 nucleic acid binding protein - like
1030 putative protein
1031 blue copper binding protein
1032 farnesylated protein (ATFP6)
1033 unknown protein
1034 putative PCF2-like DNA binding protein
1035 teosinte branched1 - like protein
1036 putative protein
1037 unknown protein
1038 unknown protein
1039 2-oxoglutarate dehydrogenase, E1 component
1040 unknown protein
1041 unknown protein
1042 CCAAT-binding transcription factor subunit A(CBF-A)
1043 hypothetical protein
1044 putative growth regulator protein
1045 putative presenilin
1046 putative expansin
1047 ribosomal - like protein
1048 unknown protein
1049 unknown protein
1050 putative protein
1051 putative protein
1052 unknown protein
1053 unknown protein
1054 unknown protein
1055 unknown protein
1056 unknown protein
1057 putative protein
1058 putative protein
1059 argininosuccinate lyase (AtArgH)
1060 disease resistance protein homolog
1061 aldehyde dehydrogenase like protein
1062 GBF2, G-box binding factor
1063 CDPK-related kinase
1064 endo-1,4-beta-glucanase
1065 putative serine protease

TABLE 1 (cont)

1066 serine/threonine-specific kinase lecRK1 precursor,lectin receptor-like
1067 putative MAP kinase
1068 RNase L inhibitor-like protein
1069 No function assigned by TIGR
1070 AP2 domain transcription factor
1071 polygalacturonase isoenzyme 1 beta subunit, putative
1072 putative lipid transfer protein
1073 putative protein kinase
1074 putative protein
1075 ATP-dependent RNA helicase like protein
1076 putative cyclic nucleotide-regulated ion channel protein
1077 COP1 like protein
1078 putative peroxidase
1079 putative NAK-like ser/thr protein kinase
1080 putative cytochrome C
1081 cytochrome c
1082 putative serine carboxypeptidase II
1083 acyl-(acyl carrier protein) thioesterase
1084 DNA-binding factor, putative
1085 MAP3K delta-1 protein kinase
1086 AtMlo-h1-like protein
1087 No function assigned by TIGR
1088 putative expansin
1089 defender against cell death protein, putative
1090 glycolate oxidase - like protein
1091 putative ATP-dependent RNA helicase
1092 putative protein
1093 putative HMG protein
1094 squalene monooxygenase 2 (squalene epoxidase 2) (SE 2) (sp|O65403)
1095 eukaryotic peptide chain release factor subunit 1, putative
1096 auxin-induced protein - like
1097 putative lipoamide dehydrogenase
1098 putative protein
1099 unknown protein
1100 putative oligopeptide transporter
1101 putative translation elongation factor ts
1102 putative CCAAT-binding transcription factor subunit
1103 putative ABC transporter
1104 putative superoxide-generating NADPH oxidase flavocytochrome
1105 aspartate kinase-homoserine dehydrogenase - like protein
1106 putative bHLH transcription factor
1107 putative geranylgeranyl transferase type I beta subunit
1108 putative ARP2/3 protein complex subunit p41
1109 sulphite reductase
1110 putative auxin-regulated protein
1111 transcription factor scarecrow-like 14, putative
1112 unknown protein
1113 monooxygenase 2 (MO2)
1114 putative amine oxidase
1115 zinc finger protein, putative
1116 DNA-binding protein, putative
1117 putative protein
1118 putative protein
1119 Avr9 elicitor response like protein
1120 putative protein
1121 hypothetical protein
1122 putative nucleotide-sugar dehydratase
1123 UFD1 like protein

TABLE 1 (cont)

1124 putative trans-prenyltransferase
1125 outward rectifying potassium channel KCO
1126 unknown protein
1127 putative pectinacetylesterase
1128 putative protein
1129 No function assigned by TIGR
1130 unknown protein
1131 unknown protein
1132 unknown protein
1133 protein phosphatase homolog (PPH1)
1134 unknown protein
1135 No function assigned by TIGR
1136 unknown protein
1137 unknown protein
1138 unknown protein
1139 putative protein
1140 unknown protein
1141 putative ubiquinol--cytochrome-c reductase
1142 unknown protein
1143 contains similarity to high-glucose-regulated protein 8 GB:AAF08813 GI:6449083 from [Homo sapiens]
1144 unknown protein
1145 putative cis-Golgi SNARE protein
1146 unknown protein
1147 glutamate-1-semialdehyde aminotransferase
1148 No function assigned by TIGR
1149 hypothetical protein
1150 unknown protein
1151 unknown protein
1152 unknown protein
1153 scarecrow-like 3
1154 putative proline-rich protein
1155 cytochrome c oxidoreductase like protein
1156 putative carboxymethylenebutenolidase
1157 unknown protein
1158 unknown protein
1159 unknown protein
1160 unknown protein
1161 unknown protein
1162 unknown protein
1163 auxin-induced protein (IAA20)
1164 50S ribosomal protein L4
1165 putative DNA topoisomerase III beta
1166 No function assigned by TIGR
1167 isp4 like protein
1168 putative protein kinase
1169 hypothetical protein
1170 putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase
1171 putative protein
1172 putative protein
1173 putative protein
1174 unknown protein
1175 unknown protein
1176 putative protein
1177 putative protein
1178 unknown protein
1179 unknown protein
1180 putative protein
1181 brassinosteroid insensitive 1 gene (BRI1)
1182 putative receptor protein kinase
1183 vacuolar-type H+-translocating inorganic pyrophosphatase
1184 protein kinase - like protein
1185 glycyl tRNA synthetase, putative
1186 subtilisin proteinase - like
1187 hypothetical protein
1188 cytochrome P450-like protein
1189 cytochrome p450 like protein
1190 putative protein kinase
1191 pectinesterase - like protein
1192 putative receptor-like protein kinase

TABLE 1 (cont)

1193 peroxidase ATP17a -like protein
1194 No function assigned by TIGR
1195 cellulose synthase catalytic subunit - like protein
1196 RAS-related protein, RAB7
1197 putative aspartate aminotransferase
1198 cyclophilin
1199 putative SF2/ASF splicing modulator, Srp30
1200 putative cytochrome b5
1201 glutamyl-tRNA reductase, putative
1202 putative MADS-box protein
1203 ammonium transport protein (AMT1)
1204 No function assigned by TIGR
1205 putative beta-ketoacyl-CoA synthase
1206 thaumatin-like protein
1207 putative methionine aminopeptidase
1208 putative protein phosphatase 2C
1209 kinase-like protein
1210 receptor-associated kinase isolog
1211 mitochondrial ribosomal protein S14
1212 oleosin, 18.5K
1213 chalcone isomerase
1214 putative cyclin-dependent kinase regulatory subunit
1215 putative thaumatin-like protein
1216 putative two-component response regulator protein
1217 TATA binding protein-associated factor, putative
1218 predicted protein of unknown function
1219 putative AP2 domain transcription factor
1220 brassinosteroid receptor kinase, putative
1221 TINY-like protein
1222 glucose-6-phosphate isomerase
1223 putative protein
1224 putative NAM (no apical meristem)-like protein
1225 unknown protein
1226 putative nucleotide-binding protein
1227 bZIP transcription factor (POSF21)
1228 ubiquitin activating enzyme - like protein
1229 telomere repeat-binding protein
1230 unknown protein
1231 mevalonate kinase
1232 putative protein
1233 hypothetical protein
1234 disease resistance RPP5 like protein
1235 putative protein
1236 putative pectinesterase
1237 Ttg1 protein (emb|CAB45372.1)
1238 FUSCA PROTEIN FUS6
1239 NHE1 Na+/H+ exchanger
1240 No function assigned by TIGR
1241 Phospholipase like protein
1242 unknown protein
1243 unknown protein
1244 unknown protein
1245 AUX1-like amino acid permease
1246 unknown protein
1247 putative C2H2-type zinc finger protein
1248 putative protein
1249 putative protein
1250 putative glucosyltransferase
1251 putative lipase
1252 putative protein
1253 putative thioredoxin
1254 AIG2-like protein
1255 short-chain alcohol dehydrogenase like protein
1256 hypothetical protein

TABLE 1 (cont)

1257 putative protein
1258 putative protein
1259 glutathione peroxidase - like protein
1260 putative protein
1261 putative disease resistance response protein
1262 putative protein
1263 senescence-associated protein (SAG29)
1264 glycolate oxidase, putative
1265 extensin - like protein
1266 putative protein
1267 unknown protein
1268 putative disease resistance protein
1269 putative receptor-like protein kinase
1270 putative receptor-like protein kinase
1271 basic chitinase
1272 putative pectin methylesterase
1273 peroxidase ATP N
1274 class 2 non-symbiotic hemoglobin
1275 nitrate transporter
1276 Ca2+/H+-exchanging protein-like
1277 putative protein
1278 hydroxynitrile lyase like protein
1279 putative AP2 domain transcription factor
1280 pectin methylesterase, putative
1281 putative protein
1282 beta-glucosidase-like protein
1283 CCAAT box binding factor/ transcription factor Hap2a
1284 putative fibrillin
1285 xyloglucan endo-transglycosylase
1286 putative 10kd chaperonin
1287 No function assigned by TIGR
1288 serine/threonine protein kinase ATPK10
1289 putative lipase
1290 choline kinase GmCK2p -like protein
1291 putative sugar transport protein, ERD6
1292 MYB27 protein - like
1293 DNA-binding protein, putative
1294 similar to cold acclimation protein WCOR413 [Triticum aestivum]
1295 unknown protein
1296 aquaporin (plasma membrane intrinsic protein 2B)
1297 No function assigned by TIGR
1298 P-Protein - like protein
1299 No function assigned by TIGR
1300 putative cytochrome P450 monooxygenase
1301 putative cytochrome P450 monooxygenase
1302 putative thioredoxin
1303 stromal ascorbate peroxidase
1304 ethylene responsive element binding factor-like protein (AtERF6)
1305 auxin transport protein EIR1 (gb|AAC39513.1)
1306 putative CONSTANS-like B-box zinc finger protein
1307 putative protein kinase
1308 mitochondrial Lon protease homolog 1 precursor (sp|O64948)
1309 putative protein
1310 heme activated protein, putative
1311 putative cytochrome P450
1312 No function assigned by TIGR
1313 putative lipase
1314 putative protein
1315 putative sugar transporter protein
1316 putative sucrose transport protein, SUC2
1317 putative protein
1318 putative protein

TABLE 1 (cont)

1319 putative endochitinase
1320 putative acetone-cyanohydrin lyase
1321 putative protein
1322 calmodulin-like protein
1323 hypothetical protein
1324 cysteine proteinase like protein
1325 heat shock protein 17.6-II
1326 heat shock protein 18
1327 Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito)
1328 unknown protein
1329 putative WRKY-type DNA binding protein
1330 No function assigned by TIGR
1331 hypothetical protein
1332 putative integral membrane protein nodulin
1333 putative protein
1334 unknown protein
1335 3-isopropylmalate dehydratase, small subunit
1336 unknown protein
1337 putative homeodomain transcription factor
1338 unknown protein
1339 putative protein
1340 peroxidase ATP19a
1341 putative Na+/H+-exchanging protein
1342 putative auxin-regulated protein
1343 unknown protein
1344 unknown protein
1345 putative trehalose-6-phosphate synthase
1346 putative lectin
1347 Mlo protein-like
1348 unknown protein
1349 ethylene response factor, putative
1350 unknown protein
1351 unknown protein
1352 bZIP transcription factor - like protein
1353 Medicago nodulin N21-like protein
1354 putative endo-1,4-beta glucanase
1355 1-aminocyclopropane-1-carboxylate oxidase
1356 putative anion exchange protein
1357 SRG1-like protein
1358 putative protein
1359 putative phi-1-like phosphate-induced protein
1360 putative protein
1361 putative embryo-abundant protein
1362 putative hydrolase
1363 unknown protein
1364 unknown protein
1365 hexose transporter - like protein
1366 unknown protein
1367 unknown protein
1368 peptide transport - like protein
1369 unknown protein
1370 putative peptide transporter
1371 disease resistance protein, putative
1372 cysteine protease component of protease-inhibitor complex
1373 putative cytochrome P450
1374 putative protein
1375 hypothetical protein
1376 unknown protein
1377 putative phosphoribosylaminoimidazolecarboxamide formyltransferase
1378 putative protein
1379 HSP like protein
1380 unknown protein
1381 unknown protein
1382 putative cytochrome P450
1383 similar to pectinesterase
1384 putative glucosyltransferase
1385 thaumatin-like protein
1386 drought-inducible cysteine proteinase RD19A precursor
1387 vegetative storage protein Vsp2
1388 unknown protein

TABLE 1 (cont)

1389 unknown protein
1390 anthranilate N-benzoyltransferase - like protein
1391 delta-1-pyrroline 5-carboxylase synthetase (P5C1)
1392 glutathione S-conjugate transporting ATPase (AtMRP1)
1393 hypothetical protein
1394 hypothetical protein
1395 unknown protein
1396 putative protein
1397 putative protein
1398 No function assigned by TIGR
1399 unknown protein
1400 putative protein kinase
1401 unknown protein
1402 hypothetical protein
1403 unknown protein
1404 putative calcium-binding EF-hand protein
1405 cinnamyl-alcohol dehydrogenase ELI3-1
1406 putative protein
1407 unknown protein
1408 senescence-associated protein sen1
1409 hypothetical protein
1410 putative cytochrome P450
1411 proline oxidase, mitochondrial precursor (osmotic stress-induced proline dehydrogenase)
1412 putative response regulator 3
1413 hypothetical protein
1414 glutamine-dependent asparagine synthetase
1415 lysine-ketoglutarate reductase/saccharopine
1416 En/Spm-like transposon protein
1417 G-box binding bZIP transcription factor
1418 putative protein
1419 putative protein
1420 putative protein
1421 ATFP4-like
1422 unknown protein
1423 unknown protein
1424 putative protein
1425 invertase inhibitor homolog (emb|CAA73335.1)
1426 unknown protein
1427 unknown protein
1428 putative cytochrome b5
1429 putative protein
1430 putative protein
1431 putative protein
1432 No function assigned by TIGR
1433 putative copper/zinc superoxide dismutase
1434 protein phosphatase ABI1
1435 glutamate dehydrogenase 2
1436 No function assigned by TIGR
1437 low-temperature-induced protein 78 (sp|Q06738)
1438 putative myo-inositol 1-phosphate synthase
1439 phosphate transporter (gb|AAB17265.1)
1440 4-hydroxyphenylpyruvate dioxygenase (HPD)
1441 histone H1
1442 hypothetical protein
1443 No function assigned by TIGR
1444 neoxanthin cleavage enzyme-like protein
1445 dehydration-induced protein RD22
1446 zinc finger protein ZAT7
1447 unknown protein
1448 unknown protein
1449 unknown protein
1450 unknown protein
1451 putative protein
1452 putative protein
1453 RNA helicase, putative

TABLE 1 (cont)

1454 putative glycine-rich protein
1455 hypothetical protein
1456 putative protein
1457 peroxidase
1458 peroxidase ATP3a (emb|CAA67340.1)
1459 metallothionein-like protein
1460 endomembrane-associated protein
1461 ferritin 1 precursor
1462 dehydrin RAB18-like protein (sp|P30185)
1463 HSR201 like protein
1464 light regulated protein, putative
1465 Dr4(protease inhibitor)
1466 mitogen activated protein kinase kinase (nMAPKK)
1467 glutathione S-transferase
1468 transcriptional activator CBF1/ CRT/CRE binding factor 1
1469 homeobox-leucine zipper protein ATHB-12
1470 amino acid permease I
1471 MAP kinase (ATMPK7)
1472 potassium channel protein AKT3
1473 cytochrome P450 monooxygenase (CYP91A2)
1474 putative transport protein
1475 putative protein
1476 hypothetical protein
1477 putative protein
1478 hypothetical protein
1479 receptor protein kinase-like protein
1480 serine/threonine protein kinase - like protein
1481 putative auxin-regulated protein
1482 amino acid transport protein AAP2
1483 unknown protein
1484 cold and ABA inducible protein kin1
1485 gamma-VPE (vacuolar processing enzyme)
1486 putative protein 1 photosystem II oxygen-evolving complex
1487 myrosinase-associated protein, putative
1488 transcription factor ATMYB4
1489 H-protein promoter binding factor-2a
1490 ammonium transporter, puitative
1491 putative zeta-carotene desaturase precursor
1492 high-affinity nitrate transporter NRT2
1493 light induced protein like
1494 putative AT-hook DNA-binding protein
1495 putative glycogenin
1496 putative light repressible receptor protein kinase
1497 serine/threonine kinase - like protein
1498 putative peroxidase
1499 cytochrome P450 monooxygenase (CYP83A1)
1500 MYB-related transcription factor (CCA1)
1501 Terminal flower1 (TFL1)
1502 sulfate transporter ATST1
1503 RING-H2 finger protein RHA3b
1504 lipoxygenase, putative
1505 serine O-acetyltransferase (EC 2.3.1.30) Sat-52 (pir||S71207)
1506 ferulate-5-hydroxylase (FAH1)
1507 En/Spm-like transposon protein, putative
1508 calmodulin-binding - like protein
1509 hypothetical protein
1510 somatic embryogenesis receptor-like kinase -like protein
1511 putative giberellin beta-hydroxylase

TABLE 1 (cont)

1512 putative pectinesterase
1513 putative protein
1514 unknown protein
1515 ribosomal protein
1516 low-temperature-induced 65 kD protein (sp|Q04980)
1517 putative glucosyltransferase
1518 peroxidase (emb|CAA67551.1)
1519 ankyrin-like protein
1520 ribosomal protein S11 - like
1521 hypothetical protein
1522 glycoprotein(EP1), putative
1523 calnexin - like protein
1524 SRG1-like protein
1525 ethylene response factor 1 (ERF1)
1526 transcriptional activator CBF1-like protein
1527 xyloglucan endo-1,4-beta-D-glucanase (XTR-6)
1528 putative cinnamyl alcohol dehydrogenase
1529 gibberellin 3 beta-hydroxylase, putative
1530 auxin response transcription factor 3 (ETTIN/ARF3)
1531 No function assigned by TIGR
1532 putative protein
1533 similar to avrRpt2-induced protein 1
1534 unknown protein
1535 hypothetical protein
1536 putative protein kinase
1537 respiratory burst oxidase - like protein
1538 glucose-6-phosphate/phosphate-translocator precursor, putative
1539 class 1 non-symbiotic hemoglobin (AHB1)
1540 endochitinase isolog
1541 putative cytochrome P450
1542 60S acidic ribosomal protein P0
1543 putative protein
1544 auxin-induced protein, putative
1545 unknown protein
1546 hypothetical protein
1547 protein phosphatase 2C ABI2 (PP2C) (sp|O04719)
1548 peroxidase, prxr2
1549 putative peroxidase ATP12a
1550 putative beta-amylase
1551 putative acetone-cyanohydrin lyase
1552 fatty acid elongase 3-ketoacyl-CoA synthase 1
1553 putative citrate synthase
1554 pEARLI 1-like protein
1555 putative MYB family transcription factor
1556 putative transcription factor MYB28
1557 RNA helicase-like protein
1558 snoRNA
1559 putative protein kinase
1560 growth regulator like protein
1561 putative potassium transporter
1562 putative protein
1563 60S ribosomal protein L14
1564 unknown protein
1565 putative RING-H2 zinc finger protein
1566 putative pollen surface protein
1567 unknown protein
1568 unknown protein
1569 unknown protein
1570 putative Ca2+-ATPase
1571 1-aminocyclopropane-1-carboxylate synthase -like protein
1572 putative beta-glucosidase
1573 transcription factor ZAP1
1574 oligopeptide transporter, putative
1575 putative protein
1576 putative glucosyltransferase
1577 putative serine/threonine kinase
1578 squalene epoxidase - like protein
1579 similar to 14KD proline-rich protein DC2.15 precursor

TABLE 1 (cont)

(sp|P14009); similar to ESTs emb|Z17709 and emb|Z47685
1580 unknown protein
1581 unknown protein
1582 hypothetical protein
1583 60S ribosomal protein L38
1584 flavin-containing monooxygenase, putative
1585 remorin
1586 unknown protein
1587 putative protein
1588 lipoxygenase
1589 cold-regulated protein COR6.6 (KIN2)
1590 Myb transcription factor homolog (ATR1)
1591 putative protein
1592 unknown protein
1593 unknown protein
1594 Ca2+-transporting ATPase - like protein
1595 protein phosphatase 2C (AtP2C-HA)
1596 peroxidase ATP24a
1597 branched-chain alpha keto-acid dehydrogenase, putative
1598 putative beta-ketoacyl-CoA synthase
1599 putative protein
1600 putative beta-galactosidase
1601 putative protein
1602 60S ribosomal protein L27
1603 putative annexin
1604 NAC domain protein, putative
1605 unknown protein
1606 late embryogenesis abundant protein LEA like
1607 unknown protein
1608 putative protein
1609 dehydrin Xero2
1610 putative zinc finger protein
1611 unknown protein
1612 DnaJ-like protein
1613 putative inositol polyphosphate-5-phosphatase
1614 putative cytochrome P450
1615 putative protein
1616 unknown protein
1617 putative protein
1618 hypothetical protein
1619 putative protein
1620 sucrose-UDP glucosyltransferase
1621 glucose-6-phosphate 1-dehydrogenase
1622 unknown protein
1623 mitochondrial chaperonin (HSP60)
1624 sucrose transport protein SUC1
1625 putative protein disulfide isomerase
1626 putative pollen-specific protein
1627 integral membrane protein, putative
1628 rubredoxin, putative
1629 putative protein
1630 disease resistance protein RPS4, putative
1631 putative peptide/amino acid transporter
1632 peroxidase, putative
1633 ethylene receptor, putative (ETR2)
1634 protein phosphatase 2C (PP2C)
1635 putative glutathione S-transferase
1636 homeodomain transcription factor (ATHB-7)
1637 putative nitrate transporter
1638 putative ribosomal protein L9, cytosolic
1639 putative DNA-binding protein
1640 beta-1,3-glucanase-like protein
1641 putative zinc transporter
1642 transcription factor TINY
1643 putative aspartate kinase-homoserine dehydrogenase
1644 ethylene reponse factor-like AP2 domain transcription factor
1645 peptide transporter - like protein
1646 trehalose-6-phosphate synthase like protein

TABLE 1 (cont)

1647 putative ribonuclease
1648 hypothetical protein
1649 putative DNA-binding protein
1650 nodulin-like protein
1651 trehalose-6-phosphate phosphatase - like protein
1652 succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1)
1653 unknown protein
1654 stress related protein, putative
1655 putative chloroplast initiation factor 3
1656 putative protein
1657 hypothetical protein
1658 putative CCCH-type zinc finger protein
1659 similar to harpin-induced protein hin1 from tobacco
1660 unknown protein
1661 unknown protein
1662 hypothetical protein
1663 No function assigned by TIGR
1664 putative protein
1665 putative glutathione S-transferase TSI-1
1666 putative protein
1667 putative PTR2 family peptide transporter
1668 receptor kinase-like protein
1669 putative sugar transport protein, ERD6
1670 putative protein
1671 nodulin-like protein
1672 unknown protein
1673 putative receptor-like protein kinase
1674 glutathione-conjugate transporter AtMRP4
1675 ascorbate oxidase-like protein
1676 pathogenesis-related protein 1 precursor, 19.3K
1677 R2R3-MYB transcription factor
1678 hypothetical protein
1679 putative chitinase
1680 Mlo protein, putative
1681 putative WRKY-type DNA binding protein
1682 putative acyl-CoA synthetase
1683 putative pathogenesis-related protein
1684 putative chitinase
1685 germin precursor oxalate oxidase
1686 endoxyloglucan transferase, putative
1687 putative protein
1688 putative cytochrome P450
1689 similar to Mlo proteins from H. vulgare
1690 putative tropinone reductase
1691 extensin-like protein
1692 putative sarcosine oxidase
1693 putative protein
1694 hypothetical protein
1695 late embryogenesis-abundant protein, putative
1696 beta-carotene hydroxylase
1697 putative calcium binding protein
1698 unknown protein
1699 unknown protein
1700 predicted glycosyl transferase
1701 hypothetical protein
1702 hypothetical protein
1703 hypothetical protein
1704 putative protein
1705 unknown protein
1706 putative protein
1707 putative protein
1708 serine/threonine kinase - like protein
1709 No function assigned by TIGR
1710 putative pectinesterase
1711 peroxidase like protein
1712 No function assigned by TIGR

TABLE 1 (cont)

1713 phenylalanine ammonia lyase (PAL1)
1714 peroxidase (emb|CAA68212.1)
1715 putative AMP deaminase
1716 putative MYB family transcription factor
1717 DNA-directed RNA polymerase II, third largest subunit
1718 nucleotide pyrophosphatase -like protein
1719 putative peroxidase
1720 calcium sensor homolog (gb|AAC26110.1)
1721 putative GDSL-motif lipase/hydrolase
1722 putative nonspecific lipid-transfer protein
1723 acyl-carrier protein (ACP), putative
1724 putative glycine dehydrogenase
1725 AIG1
1726 ACC synthase (AtACS-6)
1727 cyclin delta-3
1728 putative RING zinc finger protein
1729 aldose 1-epimerase - like protein
1730 putative phospholipase
1731 phosphoenolpyruvate carboxylase
1732 putative galactinol synthase
1733 unknown protein
1734 putative protein
1735 1-aminocyclopropane-1-carboxylate oxidase
1736 thioredoxin (clone GIF1) (pir||S58118)
1737 trehalose-6-phosphate phosphatase
1738 beta-1,3-glucanase 2 (BG2) (PR-2)
1739 putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase
1740 disease resistance protein EDS1
1741 putative protein kinase
1742 Gluthatione reductase, chloroplast precursor
1743 putative heat shock protein
1744 aspartate kinase
1745 putative major intrinsic (channel) protein
1746 matrix metalloproteinase, putative
1747 putative GDSL-motif lipase/hydrolase
1748 putative protein
1749 DAG-like protein
1750 serine/threonine kinase -like protein
1751 formamidase - like protein
1752 CER2
1753 26S proteasome subunit 4
1754 pectinesterase like protein
1755 putative disease resistance protein
1756 putative RNA methyltransferase
1757 unknown protein
1758 HOMEOBOX PROTEIN KNOTTED-1 LIKE 4 (KNAT4)
1759 glycine-rich RNA-binding protein AtGRP2 - like
1760 putative acetylornithine transaminase
1761 putative Sec24-like COPII protein
1762 putative berberine bridge enzyme
1763 putative GH3-like protein
1764 putative ABC transporter
1765 putative reticuline oxidase-like protein
1766 pectate lyase - like protein
1767 protein disulfide-isomerase-like protein
1768 putative protein
1769 putative membrane transporter
1770 unknown protein
1771 unknown protein
1772 putative RING-H2 zinc finger protein

TABLE 1 (cont)

1773 unknown protein
1774 unknown protein
1775 unknown protein
1776 MADS-box protein (AGL20)
1777 amidophosphoribosyltransferase 2 precursor
1778 putative dihydrodipicolinate synthase
1779 hypothetical protein
1780 ABA-responsive protein - like
1781 putative protein
1782 hypothetical protein
1783 DNA-binding protein-like
1784 No function assigned by TIGR
1785 transcription factor, putative
1786 nitrate reductase, putative
1787 putative protein
1788 putative protein
1789 putative protein
1790 putative protein
1791 unknown protein
1792 unknown protein
1793 tryptophan synthase beta-subunit (TSB2)
1794 hypothetical protein
1795 putative protein
1796 putative DNA-binding protein
1797 putative 40S ribosomal protein S10
1798 putative protein
1799 putative cytochrome P450
1800 putative protein
1801 putative protein
1802 putative glucosyltransferase
1803 No function assigned by TIGR
1804 putative protein
1805 putative protein
1806 unknown protein
1807 glycine-rich RNA binding protein 7
1808 dehydrin, putative
1809 putative endoxyloglucan glycosyltransferase
1810 glutamate decarboxylase 1 (GAD 1) (sp|Q42521)
1811 delta 9 desaturase
1812 UDP-glucose glucosyltransferase
1813 CARBONIC ANHYDRASE 2
1814 response reactor 2 (ATRR2)
1815 S-adenosyl-methionine-sterol-C-methyltransferase, putative
1816 putative DNA-binding protein (RAV2-like)
1817 gamma glutamyl hydrolase, putative
1818 protein phosphatase - like
1819 unknown protein
1820 unknown protein
1821 unknown protein
1822 copper transport protein - like protein
1823 hypothetical protein
1824 unknown protein
1825 putative peptide methionine sulfoxide reductase
1826 putative obtusifoliol 14-alpha demethylase
1827 glutamate dehydrogenase (EC 1.4.1.-) 1 (pir||S71217)
1828 unknown protein
1829 xyloglucan endo-1,4-beta-D-glucanase precursor
1830 unknown protein
1831 SNF1 related protein kinase (ATSRPK1)
1832 putative protein
1833 putative chloroplast nucleoid DNA binding protein
1834 hypothetical protein
1835 putative protein
1836 putative thiamin biosynthesis protein
1837 unknown protein

TABLE 1 (cont)

1838 unknown protein
1839 putative RNA helicase
1840 putative SF21 protein {Helianthus annuus}
1841 unknown protein
1842 NBS/LRR disease resistance protein, putative
1843 hypothetical protein
1844 unknown protein
1845 No function assigned by TIGR
1846 glycine-rich protein (AtGRP2)
1847 No function assigned by TIGR
1848 putative protein
1849 putative glucosyltransferase
1850 hypothetical protein
1851 hypothetical protein
1852 putative protein
1853 putative disease resistance protein
1854 thaumatin, putative
1855 putative proline-rich protein
1856 sterol-C-methyltransferase
1857 superoxidase dismutase
1858 TINY-like protein
1859 calcium-dependent protein kinase, putative
1860 hypothetical protein
1861 putative protein kinase
1862 DNA-directed RNA polymerase (mitochondrial)
1863 putaive DNA-binding protein
1864 late embryogenesis abundant M17 protein
1865 putative protein
1866 delta-1-pyrroline-5-carboxylate synthetase
1867 putative 60s ribosomal protein L10
1868 cytochrome P450 CYP86A1
1869 putative tyrosine aminotransferase
1870 thionin
1871 No function assigned by TIGR
1872 APETALA2 protein
1873 MADS-box protein (AGL3)
1874 putative monooxygenase
1875 ZFP3 zinc finger protein
1876 cell division protein FtsZ chloroplast homolog precursor (sp|Q42545)
1877 calreticulin, putative
1878 phosphoserine aminotransferase
1879 12-oxophytodienoate-10,11-reductase
1880 putative bHLH transcription factor
1881 pectin methylesterase (PMEU1), putative
1882 DNA-binding protein
1883 carnitine racemase like protein
1884 putative protein
1885 endoxyloglucan transferase (dbj|BAA81669.1)
1886 RMA1 RING zinc finger protein
1887 ammonium transporter
1888 apyrase (gb|AAF00612.1)
1889 potassium uptake transporter - like protein
1890 putative ABC transporter
1891 potassium transporter-like protein
1892 integral membrane protein, putative
1893 putative protein
1894 pyruvate decarboxylase-1 (Pdc1)
1895 putative malate oxidoreductase
1896 putative histone H2B
1897 snoRNA
1898 symbiosis-related like protein
1899 unknown protein
1900 unknown protein
1901 hypothetical protein
1902 putative protein
1903 copper-binding protein-like
1904 putative protein
1905 unknown protein
1906 putative glyoxalase II

TABLE 1 (cont)

1907 No function assigned by TIGR
1908 hypothetical protein
1909 flavanone 3-hydroxylase (FH3)
1910 putative laccase
1911 putative protein kinase
1912 myb-related protein, 33.3K (pir||S71284)
1913 unknown protein
1914 endo-xyloglucan transferase - like protein
1915 TMV resistance protein N - like
1916 putative xyloglucan endotransglycosylase
1917 unknown protein
1918 proline transporter 2
1919 resistance protein, putative
1920 actin, putative
1921 putative related to microbial divalent cation tolerance proteins
1922 unknown protein
1923 putative glycosyl transferase
1924 unknown protein
1925 putative protein phosphatase 2C
1926 unknown protein
1927 serpin, putative
1928 cinnamyl-alcohol dehydrogenase CAD1
1929 putative protein import receptor
1930 unknown protein
1931 unknown protein
1932 putative protein
1933 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
1934 unknown protein
1935 putative LRR receptor-like protein kinase
1936 serine/threonine protein kinase, putative
1937 potassium transporter - like protein
1938 lactate dehydrogenase (LDH1)
1939 hypothetical protein
1940 unknown protein
1941 putative thaumatin
1942 putative reticuline oxidase-like protein
1943 uracil phosphoribosyltransferase, putative
1944 transcription factor, putative
1945 unknown protein
1946 unknown protein
1947 GATA transcription factor 4
1948 unknown protein
1949 unknown protein
1950 senescence-associated protein -like
1951 putative pollen allergen
1952 unknown protein
1953 putative protein
1954 glycine-rich protein
1955 putative protein
1956 3-methyladenine DNA glycosylase, putative
1957 endoplasmic reticulum-type calcium-transporting ATPase 4
1958 putative pectinesterase
1959 cytochrome P450-like protein
1960 RNA-binding protein (cp33)
1961 CONSTANS-like 1
1962 putative small heat shock protein
1963 hypothetical protein
1964 unknown protein
1965 cytochrome P450 - like protein
1966 cysteine proteinase inhibitor like protein
1967 nicotianamine synthase (dbj|BAA74589.1)
1968 copper amine oxidase like protein (fragment2)
1969 putative SCARECROW gene regulator
1970 unknown protein
1971 unknown protein

TABLE 1 (cont)

1972	putative alanine acetyl transferase
1973	unknown protein
1974	unknown protein
1975	unknown protein
1976	putative extensin
1977	putative protein kinase
1978	putative protein kinase
1979	NADPH-dependent codeinone reductase, putative
1980	peroxidase
1981	putative cytochrome P450
1982	No function assigned by TIGR
1983	putative zinc-finger protein (B-box zinc finger domain)
1984	putative tyrosine aminotransferase
1985	hypothetical protein
1986	DNA binding protein
1987	putative fatty acid elongase
1988	bZIP transcription factor - like protein
1989	xyloglucan fucosyltransferase, putative
1990	unknown protein
1991	unknown protein
1992	putative protein
1993	myb factor, putative
1994	Myb-family transcription factor, putative
1995	putative fructose bisphosphate aldolase
1996	myrosinase-associated protein, putative
1997	cytochrome P450 like protein
1998	similar to SOR1 from the fungus Cercospora nicotianae
1999	similar to embryo-abundant protein GB:L47672 GI:1350530 from [Picea glauca]
2000	alcohol dehydrogenase
2001	auxin response factor 1
2002	pathogenesis-related protein 1 precursor, 18.9K
2003	hypothetical protein
2004	unknown protein
2005	zinc finger protein Zat12
2006	unknown protein
2007	unknown protein
2008	cyclin, putative
2009	2-dehydro-3-deoxyphosphoheptonate aldolase
2010	glutathione synthetase gsh2
2011	heat shock protein 17
2012	putative Na+-dependent inorganic phosphate cotransporter
2013	No function assigned by TIGR
2014	unknown protein
2015	putative protein
2016	similar to RING-H2 finger protein RHC1a GB:AAC69854 GI:3790583 from [Arabidopsis thaliana]
2017	calcium-binding protein - like
2018	putative protein
2019	putative aldehyde dehydrogenase
2020	auxin-responsive GH3 - like protein
2021	putative protein
2022	Phosphoglycerate dehydrogenase - like protein
2023	unknown protein
2024	unknown protein
2025	PSI type III chlorophyll a/b-binding protein, putative
2026	putative protein
2027	putative protein
2028	glutaredoxin, putative
2029	hypothetical protein
2030	No function assigned by TIGR
2031	putative protein
2032	jasmonate inducible protein, putative
2033	putative polygalacuronase isoenzyme 1 beta subunit
2034	putative small heat shock protein

TABLE 1 (cont)

2035 unknown protein
2036 putative disease resistance protein
2037 putative protein
2038 ethylene-responsive element binding factor, putative
2039 putative protein
2040 Pollen-specific protein precursor like
2041 putative protein
2042 unknown protein
2043 EF-Hand containing protein -like
2044 unknown protein
2045 puative calcium-transporting ATPase
2046 antifungal protein-like (PDF1.2)
2047 pathogenesis-related PR-1-like protein
2048 similar to Mlo proteins from H. vulgare
2049 putative steroid sulfotransferase
2050 trehalase - like protein
2051 thioredoxin f1
2052 unknown protein
2053 alanine-glyoxylate aminotransferase
2054 integral membrane protein, putative
2055 hypothetical protein
2056 unknown protein
2057 hypothetical protein
2058 unknown protein
2059 unknown protein
2060 unknown protein
2061 drought-induced-19-like 1
2062 unknown protein
2063 putative protein
2064 putative protein
2065 AIG2-like protein
2066 Lhca2 protein
2067 phytocyanin
2068 putative chlorophyll A-B binding protein
2069 Lhcb3 chlorophyll a/b binding protein (gb|AAD28773.1)
2070 luminal binding protein (dbj|BAA13948.1)
2071 hydroxypyruvate reductase (HPR)
2072 epoxide hydrolase (ATsEH)
2073 putative protein (fragment)
2074 unknown protein
2075 hypothetical protein
2076 putative glucosyl transferase
2077 putative glucosyl transferase
2078 putative 3-methylcrotonyl-CoA carboxylase
2079 putative peroxidase
2080 acyl-CoA oxidase (gb|AAC13497.1)
2081 alternative oxidase 1a precursor
2082 putative transcription factor (MYB4)
2083 serine acetyltransferase
2084 ATP-sulfurylase
2085 calreticulin (crt1)
2086 putative prohibitin 2
2087 putative monodehydroascorbate reductase
2088 branched-chain alpha-keto acid decarboxylase E1 beta subunit
2089 cytokinin oxidase - like protein
2090 putative receptor-like protein kinase
2091 unknown protein
2092 hypothetical protein
2093 No function assigned by TIGR
2094 putative APG protein
2095 glutathione S-transferase, putative
2096 phytochrome-associated protein 1 (PAP1)
2097 amidophosphoribosyltransferase
2098 nonphototropic hypocotyl 1
2099 3-keto-acyl-CoA thiolase 2 (gb|AAC17877.1)
2100 pEARLI 1
2101 glutathione reductase, cytosolic

TABLE 1 (cont)

2102	putative protein
2103	putative protein
2104	putative aldehyde oxidase
2105	probable photosystem I chain XI precursor
2106	photosystem II polypeptide, putative
2107	photosystem II reaction center 6.1KD protein
2108	33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb|CAA75629.1)
2109	60S ribosomal protein L11B
2110	extA (emb|CAA47807.1)
2111	zinc finger protein OBP4 - like
2112	sterol delta7 reductase
2113	putative RAS-related protein, RAB11C
2114	glucosyltransferase like protein
2115	zinc finger protein (PMZ), putative
2116	6,7-dimethyl-8-ribityllumazine synthase precursor
2117	putative protein
2118	osmotin precursor
2119	No function assigned by TIGR
2120	ferredoxin precusor isolog
2121	GH3 like protein
2122	non-specific lipid transfer protein
2123	homeodomain transcription factor (HAT9)
2124	putative cytochrome P450 monooxygenase
2125	putative protein kinase
2126	putative protein
2127	glyceraldehyde-3-phosphate dehydrogenase
2128	putative protein disulfide-isomerase
2129	unknown protein
2130	beta-1,3-glucanase class I precursor
2131	homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1)
2132	putative cyclic nucleotide-regulated ion channel protein
2133	P II nitrogen sensing protein GLB I
2134	H-protein promoter binding factor-1 (gb|AAC24592.1)
2135	GAST1-like protein
2136	cytochrome P450 GA3
2137	putative protein
2138	Myb-related transcription factor-like protein
2139	putative phloem-specific lectin
2140	protein kinase - like protein
2141	unknown protein
2142	SCARECROW transcriptional regulator-like
2143	unknown protein
2144	unknown protein
2145	putative protein
2146	calnexin homolog
2147	PP1/PP2A phosphatases pleiotropic regulator PRL2
2148	xyloglucan endotransglycosylase, putative
2149	putative calmodulin
2150	spermine synthase (ACL5)
2151	snoRNA
2152	photosystem I subunit V precursor, putative
2153	putative potassium transporter.
2154	Homeodomain - like protein
2155	putative protein
2156	unknown protein
2157	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED (TCH2)
2158	putative protein phosphatase 2C

TABLE 1 (cont)

2159 monosaccharide transport protein, STP4
2160 hypothetical protein
2161 unknown protein
2162 hypothetical protein
2163 putative protein kinase
2164 putative serine/threonine protein kinase
2165 jasmonate inducible protein, putative
2166 similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292)
2167 unknown protein
2168 MYB-like protein
2169 putative protein kinase
2170 unknown protein
2171 CLC-d chloride channel protein
2172 cytochrome P450-like protein
2173 putative glutathione S-transferase
2174 putative mandelonitrile lyase
2175 hypothetical protein
2176 putative trypsin inhibitor
2177 male sterility 2-like protein (emb|CAA68191.1)
2178 unknown protein
2179 unknown protein
2180 putative protein
2181 putative peroxidase
2182 putative thromboxane-A synthase
2183 putative cytochrome P450
2184 peroxidase ATP21a
2185 unknown protein
2186 putative glutathione S-transferase
2187 defender against cell death protein
2188 AP2 domain containing protein, putative
2189 actin depolymerizing factor - like protein
2190 putative calcium-dependent protein kinase (U90439)
2191 phosphoribosylanthranilate transferase, putative
2192 oligopeptide transporter, putative
2193 calmodulin-like protein
2194 putative protease inhibitor
2195 MAP kinase
2196 DNA binding protein MybSt1, putative
2197 putative protein
2198 putative protein
2199 unknown protein
2200 unknown protein
2201 unknown protein
2202 putative protein
2203 unknown protein
2204 unknown protein
2205 hypothetical protein
2206 uncharacterized protein
2207 putative protein
2208 hypothetical protein
2209 peroxidase (emb|CAA66967.1)
2210 putative flavonol 3-O-glucosyltransferase
2211 putative flavonol 3-O-glucosyltransferase
2212 putative protein
2213 glycerol-3-phosphate acyltransferase
2214 putative beta-1,3-glucanase
2215 putative ethylene response element binding protein (EREBP)
2216 putative CONSTANS-like B-box zinc finger protein
2217 putative protein
2218 unknown protein
2219 putative trehalose-6-phosphate phosphatase (AtTPPA)
2220 putative protein

TABLE 1 (cont)

2221 putative protein
2222 unknown protein
2223 unknown prptein
2224 unknown protein
2225 hypothetical protein
2226 putative metal-binding protein
2227 putative phosphoribosylglycinamide synthetase
2228 unknown protein
2229 putative protein
2230 unknown protein
2231 unknown protein
2232 putative beta-galactosidase
2233 putative protein kinase
2234 putative protein
2235 putative protein phosphatase 2C
2236 putative growth regulator protein
2237 putative ABC transporter
2238 chloride channel (emb|CAA70310.1)
2239 adrenodoxin - like protein
2240 NAM (no apical meristem)-like protein
2241 putative transcription factor MYB41
2242 Myb DNA binding protein - like
2243 AtMYB84
2244 photosystem II type I chlorophyll a/b binding protein
2245 putative aspartic proteinase
2246 jasmonate inducible protein, putative
2247 putative protein
2248 No function assigned by TIGR
2249 putative phosphatidylserine synthase
2250 putative nicotianamine synthase
2251 lysine and histidine specific transporter, putative
2252 putative protein
2253 putative protein
2254 putative sugar transporter protein
2255 12S cruciferin seed storage protein
2256 putative auxin-induced protein, IAA17/AXR3-1
2257 putative cyclin D
2258 farnesyl diphosphate synthase precursor (gb|AAB49290.1)
2259 putative potassium transport protein (TRH1)
2260 putative NPK1-related MAP kinase
2261 putative protein
2262 putative ABC transporter
2263 putative DNA-directed RNA polymerase subunit
2264 putative small nuclear ribonucleoprotein E
2265 unknown protein
2266 reticuline oxidase - like protein
2267 putative 1-aminocyclopropane-1-carboxylate oxidase
2268 similar to Mlo proteins from H. vulgare
2269 long-chain-fatty-acid--CoA ligase-like protein
2270 putative protein
2271 chromatin remodelling complex ATPase chain ISWI -like protein
2272 hypothetical protein
2273 latex-abundant protein, putative
2274 N-acetylornithine deacetylase-like protein, fragment
2275 putative DNA-binding protein
2276 putative anthranilate N-hydroxycinnamoyl/benzoyltransferase
2277 putative DNA binding protein
2278 cytochrome P450 - like protein
2279 putative DNA-binding protein
2280 putative peptide transporter
2281 putative reticuline oxidase-like protein

TABLE 1 (cont)

2282 thioredoxin, putative
2283 nodulin-like protein
2284 UDP-galactose transporter - like protein
2285 putative fibrillin
2286 unknown protein
2287 unknown protein
2288 unknown protein
2289 hypothetical protein
2290 glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA)
2291 predicted protein of unknown function
2292 putative protein
2293 putative protein
2294 myb-like protein
2295 hypothetical protein
2296 putative U5 small nuclear ribonucleoprotein, an RNA helicase
2297 unknown protein
2298 cinnamyl alcohol dehydrogenase - like protein
2299 hypothetical protein similar to extensin-like protein
2300 unknown protein
2301 putative chlorophyll a/b binding protein
2302 probable plasma membrane intrinsic protein 1c
2303 hexokinase (ATHXK2)
2304 calcium-dependent protein kinase
2305 5'-adenylylphosphosulfate reductase, putative
2306 Erd1 protein precursor (sp|P42762)
2307 putative protein
2308 putative protein
2309 unknown protein
2310 BCS1 protein-like protein
2311 putative protein
2312 putative protein
2313 putative protein kinase
2314 indoleacetic acid (IAA)-inducible gene (IAA7)
2315 ATP-dependent Clp protease regulatory subunit CLPX
2316 DNA-binding protein RAV1
2317 putative protein
2318 hypothetical protein
2319 unknown protein
2320 unknown protein
2321 putative protein
2322 putative thioredoxin reductase
2323 unknown protein
2324 putative lectin
2325 No function assigned by TIGR
2326 beta-fructosidase
2327 chlorophyll a/b-binding protein CP29
2328 photosystem I subunit PSI-E - like protein
2329 peroxidase ATP8a
2330 putative fructose bisphosphate aldolase
2331 zinc finger protein ATZF1, putative
2332 DegP protease precursor
2333 transcription factor-like protein
2334 calcium-dependent protein kinase
2335 hypothetical protein
2336 putative protein
2337 glucose-1-phosphate adenylyltransferase (APL3)
2338 No function assigned by TIGR
2339 putative Eukaryotic initiation factor 4A
2340 No function assigned by TIGR
2341 unknown protein
2342 beta tubulin 1, putative
2343 one helix protein (OHP)
2344 No function assigned by TIGR
2345 zinc finger protein 5, ZFP5
2346 putative MYB family transcription factor
2347 putative amino acid transporter protein

TABLE 1 (cont)

2348 putative potassium transporter
2349 protein kinase (AFC2)
2350 putative protein
2351 No function assigned by TIGR
2352 putative ubiquitin-conjugating enzyme E2
2353 unknown protein
2354 cytochrome P450 monooxygenase (CYP71B3)
2355 putative myrosinase-binding protein
2356 putative vacuolar sorting receptor
2357 uridine diphosphate glucose epimerase
2358 shaggy related protein kinase, ASK-GAMMA
2359 ankyrin repeat protein EMB506
2360 putative beta-alanine-pyruvate aminotransferase
2361 putative alcohol dehydrogenase
2362 putative receptor-like protein kinase
2363 unknown protein
2364 putative methylmalonate semi-aldehyde dehydrogenase
2365 hypothetical protein
2366 unknown protein
2367 peroxidase ATP13a
2368 putative glutathione peroxidase
2369 squamosa promoter binding protein-like 7
2370 photosystem II core complex protein, putative
2371 snoRNA
2372 photosystem I subunit X precursor
2373 MYB transcription factor (Atmyb2)
2374 putative PHD-type zinc finger protein
2375 nuclear RNA binding protein A-like protein
2376 unknown protein
2377 unknown protein
2378 unknown protein
2379 putative amino-cyclopropane-carboxylic acid oxidase (ACC oxidase)
2380 hypothetical protein
2381 indole-3-acetate beta-glucosyltransferase like protein
2382 predicted protein
2383 unknown protein
2384 No function assigned by TIGR
2385 putative photosystem I reaction center subunit IV
2386 putative homeodomain transcription factor
2387 putative purple acid phosphatase precursor
2388 No function assigned by TIGR
2389 nitrate reductase 1 (NR1)
2390 putative casein kinase II beta subunit
2391 pEARLI 1-like protein
2392 putative protein
2393 No function assigned by TIGR
2394 unknown protein
2395 putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A)
2396 unknown protein
2397 scarecrow-like 11 - like
2398 putative anthocyanidin synthase
2399 putative AP2 domain transcription factor
2400 caffeoyl-CoA O-methyltransferase - like protein
2401 unknown protein
2402 putative protein kinase
2403 cytochrome P450 -like protein
2404 putative MADS-box protein ANR1
2405 putative glutathione S-transferase

TABLE 1 (cont)

2406 hypothetical protein
2407 similar to gibberellin-regulated proteins
2408 unknown protein
2409 putative sensory transduction histidine kinase
2410 similar to late embryogenesis abundant proteins
2411 unknown protein
2412 putative protein
2413 putative ATP-dependent RNA helicase
2414 putative protein
2415 putative sucrose synthetase
2416 beta-fructofuranosidase 1
2417 putative indole-3-acetate beta-glucosyltransferase
2418 hypothetical protein
2419 DNA-directed RNA polymerase II, third largest subunit
2420 putative transcription factor
2421 homeobox-leucine zipper protein ATHB-5 (HD-zip protein ATHB-5) (sp|P46667)
2422 putative ftsH chloroplast protease
2423 replication protein A1 - like
2424 hypothetical protein
2425 unknown protein
2426 unknown protein
2427 putative methionine aminopeptidase
2428 unknown protein
2429 fatty acid elongase - like protein (cer2-like)
2430 unknown protein
2431 putative disease resistance response protein
2432 putative protein
2433 unknown protein
2434 putative protein
2435 putative protein
2436 unknown protein
2437 putative protein
2438 unknown protein
2439 unknown protein
2440 putative protein
2441 No function assigned by TIGR
2442 MADS-box protein AGL14
2443 No function assigned by TIGR
2444 peptidylprolyl isomerase
2445 putative s-adenosylmethionine synthetase
2446 peroxidase
2447 ferrochelatase-I
2448 putative eukaryotic initiation factor 4, eIF4
2449 drought-inducible cysteine proteinase RD21A precursor -like protein
2450 unknown protein
2451 unknown protein
2452 No function assigned by TIGR
2453 No function assigned by TIGR
2454 salt-inducible like protein
2455 glucose-6-phosphate 1-. dehydrogenase
2456 3-hydroxy-3-methylglutaryl CoA reductase (AA 1-592)
2457 hypothetical protein
2458 putative protein
2459 putative putative 60S ribosomal protein L17
2460 putative inorganic pyrophosphatase
2461 putative gamma-glutamyltransferase
2462 heat shock transcription factor - like protein
2463 mitochondrial chaperonin hsp60
2464 unknown protein
2465 putative zinc finger protein identical to T10M13.22
2466 putative uridylyl transferase
2467 nodulin-like protein
2468 putative B-box zinc finger protein
2469 No function assigned by TIGR
2470 putative metalloproteinase

TABLE 1 (cont)

2471 putative cellular apoptosis susceptibility protein
2472 hypothetical protein
2473 hypothetical protein
2474 scarecrow-like 13 (SCL13)
2475 putative nucleoside triphosphatase
2476 unknown protein
2477 No function assigned by TIGR
2478 hypothetical protein
2479 putative phospholipase
2480 putative snRNP protein
2481 putative protein
2482 putative lipase
2483 putative nonsense-mediated mRNA decay protein
2484 No function assigned by TIGR
2485 protochlorophyllide reductase precursor
2486 No function assigned by TIGR
2487 trehalose-6-phosphate synthase, putative
2488 unknown protein
2489 germin-like protein
2490 plastid protein
2491 putative protein
2492 hypothetical protein
2493 unknown protein
2494 unknown protein
2495 histone deacetylase-like protein
2496 unknown protein
2497 unknown protein
2498 putative protein
2499 putative protein
2500 No function assigned by TIGR
2501 putative zinc transporter ZIP2 - like
2502 unknown protein
2503 putative ribosomal-protein S6 kinase (ATPK19)
2504 unknown protein
2505 unknown protein
2506 60S ribosomal protein L10A
2507 putative protein
2508 receptor protein kinase (IRK1), putative
2509 putative nematode-resistance protein
2510 tubulin alpha-5 chain-like protein
2511 putative DNA-binding protein
2512 unknown protein
2513 putative RGA1, giberellin repsonse modulation protein
2514 non phototropic hypocotyl 1-like
2515 RING-H2 finger protein RHA1b
2516 putative myb-protein
2517 hydroperoxide lyase (HPOL) like protein
2518 serine/threonine-protein kinase, PK7
2519 putative vacuolar proton-ATPase subunit
2520 putative polygalacturonase
2521 putative ribosomal protein L8
2522 putative adenylate kinase
2523 germin-like protein (GLP10)
2524 putative chlorophyll a/b binding protein
2525 chloroplast single subunit DNA-dependent RNA polymerase
2526 putative protein
2527 hypothetical protein
2528 hypothetical protein
2529 b-keto acyl reductase, putative
2530 cellulose synthase catalytic subunit
2531 putative 1-aminocyclopropane-1-carboxylate oxidase
2532 S-linalool synthase, putative
2533 phosphoribosyl-ATP pyrophosphohydrolase (At-IE)
2534 disease resistance RPP5 like protein (fragment)
2535 putative protein
2536 beta-galactosidase like protein

TABLE 1 (cont)

2537	putative translation initiation factor eIF-2, gamma subunit
2538	ankyrin like protein
2539	histone H2A- like protein
2540	putative protein
2541	salt-tolerance zinc finger protein
2542	unknown protein
2543	putative protein
2544	fructose-bisphosphate aldolase
2545	peroxidase (emb|CAA66964.1)
2546	patatin-like protein
2547	salt-inducible protein homolog
2548	hypothetical protein
2549	xyloglucan endo-transglycosylase-like protein
2550	trihelix DNA-binding protein (GT2)
2551	ubiquitin-conjugating enzyme 16, putative
2552	homeobox protein
2553	envelope Ca2+-ATPase
2554	snap25a
2555	putative annexin
2556	putative protein
2557	homeodomain transcription factor (ATHB-14)
2558	heat shock protein, putative
2559	peroxidase ATP23a
2560	p68 RNA helicase, putative
2561	potassium transporter, putative
2562	putative eukaryotic translation initiation factor 2 alpha subunit, eIF2
2563	hypothetical protein
2564	carnitine racemase like protein
2565	No function assigned by TIGR
2566	unknown protein
2567	unknown protein
2568	unknown protein
2569	serine/threonine kinase - like protein
2570	peroxidase (emb|CAA66960.1)
2571	putative protein
2572	hypothetical protein
2573	glycine-rich protein 2 (GRP2)
2574	unknown protein
2575	berberine bridge enzyme-like protein
2576	unknown protein
2577	putative WD-repeat protein
2578	serine/threonine kinase - like protein
2579	serine /threonine kinase - like protein
2580	Cu2+-transporting ATPase-like protein
2581	translation initiation factor eIF4E
2582	O-methyltransferase - like protein
2583	translation initiation factor eIF3 - like protein
2584	No function assigned by TIGR
2585	unknown protein
2586	hypothetical protein
2587	unknown protein
2588	unknown protein
2589	glycine-rich protein like
2590	putative disease resistance protein
2591	putative Na+/Ca2+ antiporter
2592	putative hydroxymethylglutaryl-CoA lyase
2593	putative phosphoribosylaminoimidazole carboxylase
2594	SAR DNA-binding protein - like
2595	response regulator, putative
2596	fibrillin precursor-like protein
2597	beta-ketoacyl-CoA synthase (FIDDLEHEAD)
2598	lectin like protein
2599	No function assigned by TIGR

TABLE 1 (cont)

2600 acidic endochitinase (dbj|BAA21861.1)
2601 unknown protein
2602 hypothetical protein
2603 predicted OR23 protein of unknown function
2604 putative protein
2605 hypothetical protein
2606 glycerol-3-phosphate dehydrogenase
2607 hypothetical protein
2608 tat-binding protein, putative
2609 putative protein
2610 putative trehalose-6-phosphate phosphatase
2611 hypothetical protein
2612 putative flavonol 3-O-glucosyltransferase
2613 60S ribosomal protein L30
2614 putative auxin-induced protein
2615 putative nonspecific lipid-transfer protein precursor
2616 AtRer1A
2617 putative aquaporin (tonoplast intrinsic protein gamma)
2618 hypothetical protein
2619 putative alanine acetyl transferase
2620 putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
2621 putative DNA binding protein
2622 putative cystathionine gamma-synthase
2623 unknown protein
2624 malate oxidoreductase (malic enzyme)
2625 unknown protein
2626 cyclic nucleotide-gated cation channel
2627 glyoxalase II, putative
2628 putative trypsin inhibitor
2629 unknown protein
2630 unknown protein
2631 unknown protein
2632 nucleosome assembly protein I-like protein
2633 membrane channel like protein
2634 anthocyanin2, putative
2635 TWIN SISTER OF FT (TSF)
2636 putative myb-related transcription factor
2637 hypothetical protein
2638 putative RING zinc finger protein
2639 amino acid transport protein AAT1
2640 putative protein
2641 putative protein
2642 xanthine dehydrogenase
2643 xanthine dehydrogenase - like protein
2644 receptor protein kinase (IRK1), putative
2645 dehydrin-like protein
2646 unknown protein
2647 aldehyde dehydrogenase homolog, putative
2648 Ran binding protein (AtRanBP1b)
2649 putative squamosa-promoter binding protein
2650 putative protein
2651 kinesin like protein
2652 putative cellulose synthase
2653 calmodulin (cam2)
2654 fibrillarin - like protein
2655 putative transmembrane protein G5p
2656 putative peroxidase
2657 putative SNF1-related protein kinase
2658 glutathione S-transferase, putative
2659 unknown protein
2660 hypothetical protein
2661 putative protein
2662 phosphatidylinositol-4-phosphate 5-kinase isolog
2663 putative tyrosine decarboxylase
2664 unknown protein

TABLE 1 (cont)

2665 SGP1 monomeric G-protein (emb|CAB54517.1)
2666 putative serine carboxypeptidase II
2667 putative L5 ribosomal protein
2668 putative glucosyltransferase
2669 flavonoid 3,5-hydroxylase like protein
2670 putative protein
2671 putative protein
2672 putative Fe(II)/ascorbate oxidase
2673 putative anthocyanin 5-aromatic acyltransferase
2674 casein kinase I
2675 putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
2676 putative glutathione S-transferase TSI-1
2677 ATP-dependent RNA helicase
2678 putative cytochrome P450
2679 putative WD-40 repeat protein
2680 No function assigned by TIGR
2681 No function assigned by TIGR
2682 putative protein
2683 putative extensin
2684 nodulin-26 - like protein
2685 RNA helicase (emb|CAA09212.1)
2686 predicted protein of unknown function
2687 putative berberine bridge enzyme
2688 thioredoxin, putative
2689 putative serine carboxypeptidase I
2690 cytochrome P450-like protein
2691 putative pyrophosphate-dependent phosphofructokinase alpha subunit
2692 putative flavonol glucosyltransferase
2693 peroxidase ATP20a (emb|CAA67338.1)
2694 TOPP8 serine/threonine protein phosphatase type one
2695 auxin regulated protein IAA18, putative
2696 putative WRKY-type DNA binding protein
2697 putative glucan synthase
2698 squalene monooxygenase
2699 putative proline-rich protein
2700 G2484-1 protein
2701 heat shock protein 70 like protein
2702 unknown protein
2703 unknown protein

TABLE 2

ABIOTIC STRESS RESPONSIVE GENE REGULATORY SEQUENCES

SEQ ID NO:	REGULATORY REGION	SEQ ID NO:	REGULATORY REGION	SEQ ID NO:	REGULATORY REGION
1	2704	51	2753	101	2802
2	2705	52	2754	102	2803
3	2706	53	2755	103	2804
4	2707	54	2756	104	2805
5	2708	55	2757	105	2806
6	2709	56	2758	106	2807
7	2710	57	2759	107	2808
8	2711	58	2760	108	2809
9	2712	59	2761	109	2810
10	2713	60	2762	110	2811
11	2714	61	2763	111	2812
12	2715	62	2764	112	2813
13	2716	63	2765	113	2814
14	2717	64	2766	114	2815
15	2718	65	2767	115	2816
16	2719	66	2768	116	2817
17	2720	67	2769	117	2818
18	2721	68	2770	118	2819
19	2722	69	NONE	119	2820
20	2723	70	2771	120	2821
21	2724	71	2772	121	2822
22	2725	72	2773	122	2823
23	2726	73	2774	123	2824
24	2727	74	2775	124	2825
25	2728	75	2776	125	2826
26	2729	76	2777	126	2827
27	2730	77	2778	127	2828
28	2731	78	2779	128	2829
29	2732	79	2780	129	2830
30	2733	80	2781	130	2831
31	2734	81	2782	131	2832
32	2735	82	2783	132	2833
33	2736	83	2784	133	2834
34	2737	84	2785	134	2835
35	2738	85	2786	135	2836
36	2739	86	2787	136	2837
37	2740	87	2788	137	2838
38	2741	88	2789	138	2839
39	2742	89	2790	139	2840
40	2743	90	2791	140	2841
41	2744	91	2792	141	2842
42	2745	92	2793	142	2843
43	NONE	93	2794	143	2844
44	2746	94	2795	144	NONE
45	2747	95	2796	145	2845
46	2748	96	2797	146	2846
47	2749	97	2798	147	2847
48	2750	98	2799	148	2848
49	2751	99	2800	149	2849
50	2752	100	2801	150	2850

TABLE 2 (cont)

151	2851	205	2905	259	2959
152	2852	206	2906	260	2960
153	2853	207	2907	261	2961
154	2854	208	2908	262	2962
155	2855	209	2909	263	2963
156	2856	210	2910	264	2964
157	2857	211	2911	265	2965
158	2858	212	2912	266	2966
159	2859	213	2913	267	2967
160	2860	214	2914	268	2968
161	2861	215	2915	269	2969
162	2862	216	2916	270	2970
163	2863	217	2917	271	2971
164	2864	218	2918	272	2972
165	2865	219	2919	273	2973
166	2866	220	2920	274	2974
167	2867	221	2921	275	2975
168	2868	222	2922	276	2976
169	2869	223	2923	277	2977
170	2870	224	2924	278	2978
171	2871	225	2925	279	2979
172	2872	226	2926	280	2980
173	2873	227	2927	281	2981
174	2874	228	2928	282	2982
175	2875	229	2929	283	2983
176	2876	230	2930	284	2984
177	2877	231	2931	285	2985
178	2878	232	2932	286	2986
179	2879	233	2933	287	2987
180	2880	234	2934	288	2988
181	2881	235	2935	289	2989
182	2882	236	2936	290	2990
183	2883	237	2937	291	2991
184	2884	238	2938	292	2992
185	2885	239	2939	293	2993
186	2886	240	2940	294	2994
187	2887	241	2941	295	2995
188	2888	242	2942	296	2996
189	2889	243	2943	297	2997
190	2890	244	2944	298	2998
191	2891	245	2945	299	2999
192	2892	246	2946	300	3000
193	2893	247	2947	301	3001
194	2894	248	2948	302	3002
195	2895	249	2949	303	3003
196	2896	250	2950	304	NONE
197	2897	251	2951	305	3004
198	2898	252	2952	306	3005
199	2899	253	2953	307	3006
200	2900	254	2954	308	3007
201	2901	255	2955	309	3008
202	2902	256	2956	310	3009
203	2903	257	2957	311	3010
204	2904	258	2958	312	3011

TABLE 2 (cont)

313	3012	367	3066	421	3120
314	3013	368	3067	422	3121
315	3014	369	3068	423	3122
316	3015	370	3069	424	3123
317	3016	371	3070	425	3124
318	3017	372	3071	426	3125
319	3018	373	3072	427	3126
320	3019	374	3073	428	3127
321	3020	375	3074	429	3128
322	3021	376	3075	430	3129
323	3022	377	3076	431	3130
324	3023	378	3077	432	3131
325	3024	379	3078	433	3132
326	3025	380	3079	434	3133
327	3026	381	3080	435	3134
328	3027	382	3081	436	3135
329	3028	383	3082	437	3136
330	3029	384	3083	438	3137
331	3030	385	3084	439	3138
332	3031	386	3085	440	3139
333	3032	387	3086	441	3140
334	3033	388	3087	442	3141
335	3034	389	3088	443	3142
336	3035	390	3089	444	3143
337	3036	391	3090	445	3144
338	3037	392	3091	446	3145
339	3038	393	3092	447	3146
340	3039	394	3093	448	3147
341	3040	395	3094	449	3148
342	3041	396	3095	450	3149
343	3042	397	3096	451	3150
344	3043	398	3097	452	3151
345	3044	399	3098	453	3152
346	3045	400	3099	454	3153
347	3046	401	3100	455	3154
348	3047	402	3101	456	3155
349	3048	403	3102	457	3156
350	3049	404	3103	458	3157
351	3050	405	3104	459	3158
352	3051	406	3105	460	3159
353	3052	407	3106	461	3160
354	3053	408	3107	462	3161
355	3054	409	3108	463	3162
356	3055	410	3109	464	3163
357	3056	411	3110	465	3164
358	3057	412	3111	466	3165
359	3058	413	3112	467	3166
360	3059	414	3113	468	3167
361	3060	415	3114	469	3168
362	3061	416	3115	470	3169
363	3062	417	3116	471	3170
364	3063	418	3117	472	3171
365	3064	419	3118	473	3172
366	3065	420	3119	474	3173

TABLE 2 (cont)

475	3174	529	3228	583	3282
476	3175	530	3229	584	3283
477	3176	531	3230	585	3284
478	3177	532	3231	586	3285
479	3178	533	3232	587	3286
480	3179	534	3233	588	3287
481	3180	535	3234	589	3288
482	3181	536	3235	590	3289
483	3182	537	3236	591	3290
484	3183	538	3237	592	3291
485	3184	539	3238	593	3292
486	3185	540	3239	594	3293
487	3186	541	3240	595	3294
488	3187	542	3241	596	3295
489	3188	543	3242	597	3296
490	3189	544	3243	598	3297
491	3190	545	3244	599	3298
492	3191	546	3245	600	3299
493	3192	547	3246	601	3300
494	3193	548	3247	602	3301
495	3194	549	3248	603	3302
496	3195	550	3249	604	3303
497	3196	551	3250	605	3304
498	3197	552	3251	606	3305
499	3198	553	3252	607	3306
500	3199	554	3253	608	3307
501	3200	555	3254	609	3308
502	3201	556	3255	610	3309
503	3202	557	3256	611	3310
504	3203	558	3257	612	3311
505	3204	559	3258	613	3312
506	3205	560	3259	614	3313
507	3206	561	3260	615	3314
508	3207	562	3261	616	3315
509	3208	563	3262	617	3316
510	3209	564	3263	618	3317
511	3210	565	3264	619	3318
512	3211	566	3265	620	3319
513	3212	567	3266	621	3320
514	3213	568	3267	622	3321
515	3214	569	3268	623	3322
516	3215	570	3269	624	3323
517	3216	571	3270	625	3324
518	3217	572	3271	626	3325
519	3218	573	3272	627	3326
520	3219	574	3273	628	3327
521	3220	575	3274	629	3328
522	3221	576	3275	630	3329
523	3222	577	3276	631	3330
524	3223	578	3277	632	3331
525	3224	579	3278	633	3332
526	3225	580	3279	634	3333
527	3226	581	3280	635	3334
528	3227	582	3281	636	3335

TABLE 2 (cont)

637	3336	691	3390	745	3444
638	3337	692	3391	746	3445
639	3338	693	3392	747	3446
640	3339	694	3393	748	3447
641	3340	695	3394	749	3448
642	3341	696	3395	750	3449
643	3342	697	3396	751	3450
644	3343	698	3397	752	3451
645	3344	699	3398	753	3452
646	3345	700	3399	754	3453
647	3346	701	3400	755	3454
648	3347	702	3401	756	3455
649	3348	703	3402	757	3456
650	3349	704	3403	758	3457
651	3350	705	3404	759	3458
652	3351	706	3405	760	3459
653	3352	707	3406	761	3460
654	3353	708	3407	762	3461
655	3354	709	3408	763	3462
656	3355	710	3409	764	3463
657	3356	711	3410	765	3464
658	3357	712	3411	766	3465
659	3358	713	3412	767	3466
660	3359	714	3413	768	3467
661	3360	715	3414	769	3468
662	3361	716	3415	770	3469
663	3362	717	3416	771	3470
664	3363	718	3417	772	3471
665	3364	719	3418	773	3472
666	3365	720	3419	774	3473
667	3366	721	3420	775	3474
668	3367	722	3421	776	3475
669	3368	723	3422	777	3476
670	3369	724	3423	778	3477
671	3370	725	3424	779	3478
672	3371	726	3425	780	3479
673	3372	727	3426	781	3480
674	3373	728	3427	782	3481
675	3374	729	3428	783	3482
676	3375	730	3429	784	3483
677	3376	731	3430	785	3484
678	3377	732	3431	786	3485
679	3378	733	3432	787	3486
680	3379	734	3433	788	3487
681	3380	735	3434	789	3488
682	3381	736	3435	790	3489
683	3382	737	3436	791	3490
684	3383	738	3437	792	3491
685	3384	739	3438	793	3492
686	3385	740	3439	794	3493
687	3386	741	3440	795	3494
688	3387	742	3441	796	3495
689	3388	743	3442	797	3496
690	3389	744	3443	798	3497

TABLE 2 (cont)

799	3498	853	3552	907	3603
800	3499	854	3553	908	3604
801	3500	855	3554	909	3605
802	3501	856	3555	910	3606
803	3502	857	3556	911	3607
804	3503	858	3557	912	3608
805	3504	859	3558	913	3609
806	3505	860	3559	914	3610
807	3506	861	3560	915	3611
808	3507	862	3561	916	3612
809	3508	863	3562	917	3613
810	3509	864	3563	918	3614
811	3510	865	3564	919	3615
812	3511	866	3565	920	3616
813	3512	867	3566	921	3617
814	3513	868	3567	922	3618
815	3514	869	3568	923	3619
816	3515	870	3569	924	3620
817	3516	871	3570	925	3621
818	3517	872	3571	926	3622
819	3518	873	3572	927	3623
820	3519	874	3573	928	3624
821	3520	875	3574	929	3625
822	3521	876	3575	930	3626
823	3522	877	3576	931	3627
824	3523	878	3577	932	3628
825	3524	879	3578	933	3629
826	3525	880	3579	934	3630
827	3526	881	3580	935	NONE
828	3527	882	3581	936	3631
829	3528	883	3582	937	3632
830	3529	884	3583	938	3633
831	3530	885	3584	939	3634
832	3531	886	3585	940	3635
833	3532	887	NONE	941	3636
834	3533	888	3586	942	3637
835	3534	889	3587	943	3638
836	3535	890	3588	944	3639
837	3536	891	3589	945	3640
838	3537	892	3590	946	3641
839	3538	893	3591	947	3642
840	3539	894	NONE	948	3643
841	3540	895	NONE	949	3644
842	3541	896	3592	950	3645
843	3542	897	3593	951	3646
844	3543	898	3594	952	3647
845	3544	899	3595	953	3648
846	3545	900	3596	954	3649
847	3546	901	3597	955	3650
848	3547	902	3598	956	3651
849	3548	903	3599	957	3652
850	3549	904	3600	958	3653
851	3550	905	3601	959	3654
852	3551	906	3602	960	3655

TABLE 2 (cont)

961	3656	1015	3710	1069	3764
962	3657	1016	3711	1070	3765
963	3658	1017	3712	1071	3766
964	3659	1018	3713	1072	3767
965	3660	1019	3714	1073	3768
966	3661	1020	3715	1074	3769
967	3662	1021	3716	1075	3770
968	3663	1022	3717	1076	3771
969	3664	1023	3718	1077	3772
970	3665	1024	3719	1078	3773
971	3666	1025	3720	1079	3774
972	3667	1026	3721	1080	3775
973	3668	1027	3722	1081	3776
974	3669	1028	3723	1082	3777
975	3670	1029	3724	1083	3778
976	3671	1030	3725	1084	3779
977	3672	1031	3726	1085	3780
978	3673	1032	3727	1086	3781
979	3674	1033	3728	1087	NONE
980	3675	1034	3729	1088	3782
981	3676	1035	3730	1089	3783
982	3677	1036	3731	1090	3784
983	3678	1037	3732	1091	3785
984	3679	1038	3733	1092	3786
985	3680	1039	3734	1093	3787
986	3681	1040	3735	1094	3788
987	3682	1041	3736	1095	3789
988	3683	1042	3737	1096	3790
989	3684	1043	3738	1097	3791
990	3685	1044	3739	1098	3792
991	3686	1045	3740	1099	3793
992	3687	1046	3741	1100	3794
993	3688	1047	3742	1101	3795
994	3689	1048	3743	1102	3796
995	3690	1049	3744	1103	3797
996	3691	1050	3745	1104	3798
997	3692	1051	3746	1105	3799
998	3693	1052	3747	1106	3800
999	3694	1053	3748	1107	3801
1000	3695	1054	3749	1108	3802
1001	3696	1055	3750	1109	3803
1002	3697	1056	3751	1110	3804
1003	3698	1057	3752	1111	3805
1004	3699	1058	3753	1112	3806
1005	3700	1059	3754	1113	3807
1006	3701	1060	3755	1114	3808
1007	3702	1061	3756	1115	3809
1008	3703	1062	3757	1116	3810
1009	3704	1063	3758	1117	3811
1010	3705	1064	3759	1118	3812
1011	3706	1065	3760	1119	3813
1012	3707	1066	3761	1120	3814
1013	3708	1067	3762	1121	3815
1014	3709	1068	3763	1122	3816

TABLE 2 (cont)

1123	3817	1177	3871	1231	3925
1124	3818	1178	3872	1232	3926
1125	3819	1179	3873	1233	3927
1126	3820	1180	3874	1234	3928
1127	3821	1181	3875	1235	3929
1128	3822	1182	3876	1236	3930
1129	3823	1183	3877	1237	3931
1130	3824	1184	3878	1238	3932
1131	3825	1185	3879	1239	3933
1132	3826	1186	3880	1240	3934
1133	3827	1187	3881	1241	3935
1134	3828	1188	3882	1242	3936
1135	3829	1189	3883	1243	3937
1136	3830	1190	3884	1244	3938
1137	3831	1191	3885	1245	3939
1138	3832	1192	3886	1246	3940
1139	3833	1193	3887	1247	3941
1140	3834	1194	3888	1248	3942
1141	3835	1195	3889	1249	3943
1142	3836	1196	3890	1250	3944
1143	3837	1197	3891	1251	3945
1144	3838	1198	3892	1252	3946
1145	3839	1199	3893	1253	3947
1146	3840	1200	3894	1254	3948
1147	3841	1201	3895	1255	3949
1148	3842	1202	3896	1256	3950
1149	3843	1203	3897	1257	3951
1150	3844	1204	3898	1258	3952
1151	3845	1205	3899	1259	3953
1152	3846	1206	3900	1260	3954
1153	3847	1207	3901	1261	3955
1154	3848	1208	3902	1262	3956
1155	3849	1209	3903	1263	3957
1156	3850	1210	3904	1264	3958
1157	3851	1211	3905	1265	3959
1158	3852	1212	3906	1266	3960
1159	3853	1213	3907	1267	3961
1160	3854	1214	3908	1268	3962
1161	3855	1215	3909	1269	3963
1162	3856	1216	3910	1270	3964
1163	3857	1217	3911	1271	3965
1164	3858	1218	3912	1272	3966
1165	3859	1219	3913	1273	3967
1166	3860	1220	3914	1274	3968
1167	3861	1221	3915	1275	3969
1168	3862	1222	3916	1276	3970
1169	3863	1223	3917	1277	3971
1170	3864	1224	3918	1278	3972
1171	3865	1225	3919	1279	3973
1172	3866	1226	3920	1280	3974
1173	3867	1227	3921	1281	3975
1174	3868	1228	3922	1282	3976
1175	3869	1229	3923	1283	3977
1176	3870	1230	3924	1284	3978

TABLE 2 (cont)

1285	3979	1339	4032	1393	4086
1286	3980	1340	4033	1394	4087
1287	3981	1341	4034	1395	4088
1288	3982	1342	4035	1396	4089
1289	3983	1343	4036	1397	4090
1290	3984	1344	4037	1398	4091
1291	3985	1345	4038	1399	4092
1292	3986	1346	4039	1400	4093
1293	3987	1347	4040	1401	4094
1294	3988	1348	4041	1402	4095
1295	3989	1349	4042	1403	4096
1296	3990	1350	4043	1404	4097
1297	3991	1351	4044	1405	4098
1298	3992	1352	4045	1406	4099
1299	3993	1353	4046	1407	4100
1300	3994	1354	4047	1408	4101
1301	3995	1355	4048	1409	4102
1302	3996	1356	4049	1410	4103
1303	3997	1357	4050	1411	4104
1304	3998	1358	4051	1412	4105
1305	3999	1359	4052	1413	4106
1306	4000	1360	4053	1414	4107
1307	4001	1361	4054	1415	4108
1308	4002	1362	4055	1416	4109
1309	4003	1363	4056	1417	4110
1310	4004	1364	4057	1418	4111
1311	4005	1365	4058	1419	4112
1312	4006	1366	4059	1420	4113
1313	4007	1367	4060	1421	4114
1314	4008	1368	4061	1422	4115
1315	4009	1369	4062	1423	4116
1316	4010	1370	4063	1424	4117
1317	4011	1371	4064	1425	4118
1318	4012	1372	4065	1426	4119
1319	4013	1373	4066	1427	4120
1320	4014	1374	4067	1428	4121
1321	4015	1375	4068	1429	4122
1322	4016	1376	4069	1430	4123
1323	4017	1377	4070	1431	4124
1324	4018	1378	4071	1432	NONE
1325	4019	1379	4072	1433	4125
1326	4020	1380	4073	1434	4126
1327	4021	1381	4074	1435	4127
1328	4022	1382	4075	1436	4128
1329	4023	1383	4076	1437	4129
1330	NONE	1384	4077	1438	4130
1331	4024	1385	4078	1439	4131
1332	4025	1386	4079	1440	4132
1333	4026	1387	4080	1441	4133
1334	4027	1388	4081	1442	4134
1335	4028	1389	4082	1443	4135
1336	4029	1390	4083	1444	4136
1337	4030	1391	4084	1445	4137
1338	4031	1392	4085	1446	4138

TABLE 2 (cont)

1447	4139	1501	4193	1555	4247
1448	4140	1502	4194	1556	4248
1449	4141	1503	4195	1557	4249
1450	4142	1504	4196	1558	NONE
1451	4143	1505	4197	1559	4250
1452	4144	1506	4198	1560	4251
1453	4145	1507	4199	1561	4252
1454	4146	1508	4200	1562	4253
1455	4147	1509	4201	1563	4254
1456	4148	1510	4202	1564	4255
1457	4149	1511	4203	1565	4256
1458	4150	1512	4204	1566	4257
1459	4151	1513	4205	1567	4258
1460	4152	1514	4206	1568	4259
1461	4153	1515	4207	1569	4260
1462	4154	1516	4208	1570	4261
1463	4155	1517	4209	1571	4262
1464	4156	1518	4210	1572	4263
1465	4157	1519	4211	1573	4264
1466	4158	1520	4212	1574	4265
1467	4159	1521	4213	1575	4266
1468	4160	1522	4214	1576	4267
1469	4161	1523	4215	1577	4268
1470	4162	1524	4216	1578	4269
1471	4163	1525	4217	1579	4270
1472	4164	1526	4218	1580	4271
1473	4165	1527	4219	1581	4272
1474	4166	1528	4220	1582	4273
1475	4167	1529	4221	1583	4274
1476	4168	1530	4222	1584	4275
1477	4169	1531	4223	1585	4276
1478	4170	1532	4224	1586	4277
1479	4171	1533	4225	1587	4278
1480	4172	1534	4226	1588	4279
1481	4173	1535	4227	1589	4280
1482	4174	1536	4228	1590	4281
1483	4175	1537	4229	1591	4282
1484	4176	1538	4230	1592	4283
1485	4177	1539	4231	1593	4284
1486	4178	1540	4232	1594	4285
1487	4179	1541	4233	1595	4286
1488	4180	1542	4234	1596	4287
1489	4181	1543	4235	1597	4288
1490	4182	1544	4236	1598	4289
1491	4183	1545	4237	1599	4290
1492	4184	1546	4238	1600	4291
1493	4185	1547	4239	1601	4292
1494	4186	1548	4240	1602	4293
1495	4187	1549	4241	1603	4294
1496	4188	1550	4242	1604	4295
1497	4189	1551	4243	1605	4296
1498	4190	1552	4244	1606	4297
1499	4191	1553	4245	1607	4298
1500	4192	1554	4246	1608	4299

TABLE 2 (cont)

1609	4300	1663	NONE	1717	4406
1610	4301	1664	4354	1718	4407
1611	4302	1665	4355	1719	4408
1612	4303	1666	4356	1720	4409
1613	4304	1667	4357	1721	4410
1614	4305	1668	4358	1722	4411
1615	4306	1669	4359	1723	4412
1616	4307	1670	4360	1724	4413
1617	4308	1671	4361	1725	4414
1618	4309	1672	4362	1726	4415
1619	4310	1673	4363	1727	4416
1620	4311	1674	4364	1728	4417
1621	4312	1675	4365	1729	4418
1622	4313	1676	4366	1730	4419
1623	4314	1677	4367	1731	4420
1624	4315	1678	4368	1732	4421
1625	4316	1679	4369	1733	4422
1626	4317	1680	4370	1734	4423
1627	4318	1681	4371	1735	4424
1628	4319	1682	4372	1736	4425
1629	4320	1683	4373	1737	4426
1630	4321	1684	4374	1738	4427
1631	4322	1685	4375	1739	4428
1632	4323	1686	4376	1740	4429
1633	4324	1687	4377	1741	4430
1634	4325	1688	4378	1742	4431
1635	4326	1689	4379	1743	4432
1636	4327	1690	4380	1744	4433
1637	4328	1691	4381	1745	4434
1638	4329	1692	4382	1746	4435
1639	4330	1693	4383	1747	4436
1640	4331	1694	4384	1748	4437
1641	4332	1695	4385	1749	4438
1642	4333	1696	4386	1750	4439
1643	4334	1697	4387	1751	4440
1644	4335	1698	4388	1752	4441
1645	4336	1699	4389	1753	4442
1646	4337	1700	4390	1754	4443
1647	4338	1701	4391	1755	4444
1648	4339	1702	4392	1756	4445
1649	4340	1703	4393	1757	4446
1650	4341	1704	4394	1758	4447
1651	4342	1705	4395	1759	4448
1652	4343	1706	4396	1760	4449
1653	4344	1707	4397	1761	4450
1654	4345	1708	4398	1762	4451
1655	4346	1709	4399	1763	4452
1656	4347	1710	4400	1764	4453
1657	4348	1711	4401	1765	4454
1658	4349	1712	NONE	1766	4455
1659	4350	1713	4402	1767	4456
1660	4351	1714	4403	1768	4457
1661	4352	1715	4404	1769	4458
1662	4353	1716	4405	1770	4459

TABLE 2 (cont)

1771	4460	1825	4512	1879	4566
1772	4461	1826	4513	1880	4567
1773	4462	1827	4514	1881	4568
1774	4463	1828	4515	1882	4569
1775	4464	1829	4516	1883	4570
1776	4465	1830	4517	1884	4571
1777	4466	1831	4518	1885	4572
1778	4467	1832	4519	1886	4573
1779	4468	1833	4520	1887	4574
1780	4469	1834	4521	1888	4575
1781	4470	1835	4522	1889	4576
1782	4471	1836	4523	1890	4577
1783	4472	1837	4524	1891	4578
1784	NONE	1838	4525	1892	4579
1785	4473	1839	4526	1893	4580
1786	4474	1840	4527	1894	4581
1787	4475	1841	4528	1895	4582
1788	4476	1842	4529	1896	4583
1789	4477	1843	4530	1897	NONE
1790	4478	1844	4531	1898	4584
1791	4479	1845	4532	1899	4585
1792	4480	1846	4533	1900	4586
1793	4481	1847	4534	1901	4587
1794	4482	1848	4535	1902	4588
1795	4483	1849	4536	1903	4589
1796	4484	1850	4537	1904	4590
1797	4485	1851	4538	1905	4591
1798	4486	1852	4539	1906	4592
1799	4487	1853	4540	1907	NONE
1800	4488	1854	4541	1908	4593
1801	4489	1855	4542	1909	4594
1802	4490	1856	4543	1910	4595
1803	NONE	1857	4544	1911	4596
1804	4491	1858	4545	1912	4597
1805	4492	1859	4546	1913	4598
1806	4493	1860	4547	1914	4599
1807	4494	1861	4548	1915	4600
1808	4495	1862	4549	1916	4601
1809	4496	1863	4550	1917	4602
1810	4497	1864	4551	1918	4603
1811	4498	1865	4552	1919	4604
1812	4499	1866	4553	1920	4605
1813	4500	1867	4554	1921	4606
1814	4501	1868	4555	1922	4607
1815	4502	1869	4556	1923	4608
1816	4503	1870	4557	1924	4609
1817	4504	1871	4558	1925	4610
1818	4505	1872	4559	1926	4611
1819	4506	1873	4560	1927	4612
1820	4507	1874	4561	1928	4613
1821	4508	1875	4562	1929	4614
1822	4509	1876	4563	1930	4615
1823	4510	1877	4564	1931	4616
1824	4511	1878	4565	1932	4617

TABLE 2 (cont)

1933	4618	1987	4672	2041	4725
1934	4619	1988	4673	2042	4726
1935	4620	1989	4674	2043	4727
1936	4621	1990	4675	2044	4728
1937	4622	1991	4676	2045	4729
1938	4623	1992	4677	2046	4730
1939	4624	1993	4678	2047	4731
1940	4625	1994	4679	2048	4732
1941	4626	1995	4680	2049	4733
1942	4627	1996	4681	2050	4734
1943	4628	1997	4682	2051	4735
1944	4629	1998	4683	2052	4736
1945	4630	1999	4684	2053	4737
1946	4631	2000	4685	2054	4738
1947	4632	2001	4686	2055	4739
1948	4633	2002	4687	2056	4740
1949	4634	2003	4688	2057	4741
1950	4635	2004	4689	2058	4742
1951	4636	2005	4690	2059	4743
1952	4637	2006	4691	2060	4744
1953	4638	2007	4692	2061	4745
1954	4639	2008	4693	2062	4746
1955	4640	2009	4694	2063	4747
1956	4641	2010	4695	2064	4748
1957	4642	2011	4696	2065	4749
1958	4643	2012	4697	2066	4750
1959	4644	2013	4698	2067	4751
1960	4645	2014	4699	2068	4752
1961	4646	2015	4700	2069	4753
1962	4647	2016	4701	2070	4754
1963	4648	2017	4702	2071	4755
1964	4649	2018	4703	2072	4756
1965	4650	2019	4704	2073	4757
1966	4651	2020	4705	2074	4758
1967	4652	2021	4706	2075	4759
1968	4653	2022	4707	2076	4760
1969	4654	2023	4708	2077	4761
1970	4655	2024	4709	2078	4762
1971	4656	2025	4710	2079	4763
1972	4657	2026	4711	2080	4764
1973	4658	2027	4712	2081	4765
1974	4659	2028	4713	2082	4766
1975	4660	2029	4714	2083	4767
1976	4661	2030	NONE	2084	4768
1977	4662	2031	4715	2085	4769
1978	4663	2032	4716	2086	4770
1979	4664	2033	4717	2087	4771
1980	4665	2034	4718	2088	4772
1981	4666	2035	4719	2089	4773
1982	4667	2036	4720	2090	4774
1983	4668	2037	4721	2091	4775
1984	4669	2038	4722	2092	4776
1985	4670	2039	4723	2093	4777
1986	4671	2040	4724	2094	4778

TABLE 2 (cont)

2095	4779	2149	4833	2203	4886
2096	4780	2150	4834	2204	4887
2097	4781	2151	NONE	2205	4888
2098	4782	2152	4835	2206	4889
2099	4783	2153	4836	2207	4890
2100	4784	2154	4837	2208	4891
2101	4785	2155	4838	2209	4892
2102	4786	2156	4839	2210	4893
2103	4787	2157	4840	2211	4894
2104	4788	2158	4841	2212	4895
2105	4789	2159	4842	2213	4896
2106	4790	2160	4843	2214	4897
2107	4791	2161	4844	2215	4898
2108	4792	2162	4845	2216	4899
2109	4793	2163	4846	2217	4900
2110	4794	2164	4847	2218	4901
2111	4795	2165	4848	2219	4902
2112	4796	2166	4849	2220	4903
2113	4797	2167	4850	2221	4904
2114	4798	2168	4851	2222	4905
2115	4799	2169	4852	2223	4906
2116	4800	2170	4853	2224	4907
2117	4801	2171	4854	2225	4908
2118	4802	2172	4855	2226	4909
2119	4803	2173	4856	2227	4910
2120	4804	2174	4857	2228	4911
2121	4805	2175	4858	2229	4912
2122	4806	2176	4859	2230	4913
2123	4807	2177	4860	2231	4914
2124	4808	2178	4861	2232	4915
2125	4809	2179	4862	2233	4916
2126	4810	2180	4863	2234	4917
2127	4811	2181	4864	2235	4918
2128	4812	2182	4865	2236	4919
2129	4813	2183	4866	2237	4920
2130	4814	2184	4867	2238	4921
2131	4815	2185	4868	2239	4922
2132	4816	2186	4869	2240	4923
2133	4817	2187	4870	2241	4924
2134	4818	2188	4871	2242	4925
2135	4819	2189	4872	2243	4926
2136	4820	2190	4873	2244	4927
2137	4821	2191	4874	2245	4928
2138	4822	2192	4875	2246	4929
2139	4823	2193	4876	2247	4930
2140	4824	2194	4877	2248	NONE
2141	4825	2195	4878	2249	4931
2142	4826	2196	4879	2250	4932
2143	4827	2197	4880	2251	4933
2144	4828	2198	4881	2252	4934
2145	4829	2199	4882	2253	4935
2146	4830	2200	4883	2254	4936
2147	4831	2201	4884	2255	4937
2148	4832	2202	4885	2256	4938

TABLE 2 (cont)

2257	4939	2311	4993	2365	5046
2258	4940	2312	4994	2366	5047
2259	4941	2313	4995	2367	5048
2260	4942	2314	4996	2368	5049
2261	4943	2315	4997	2369	5050
2262	4944	2316	4998	2370	5051
2263	4945	2317	4999	2371	NONE
2264	4946	2318	5000	2372	5052
2265	4947	2319	5001	2373	5053
2266	4948	2320	5002	2374	5054
2267	4949	2321	5003	2375	5055
2268	4950	2322	5004	2376	5056
2269	4951	2323	5005	2377	5057
2270	4952	2324	5006	2378	5058
2271	4953	2325	5007	2379	5059
2272	4954	2326	5008	2380	5060
2273	4955	2327	5009	2381	5061
2274	4956	2328	5010	2382	5062
2275	4957	2329	5011	2383	5063
2276	4958	2330	5012	2384	5064
2277	4959	2331	5013	2385	5065
2278	4960	2332	5014	2386	5066
2279	4961	2333	5015	2387	5067
2280	4962	2334	5016	2388	5068
2281	4963	2335	5017	2389	5069
2282	4964	2336	5018	2390	5070
2283	4965	2337	5019	2391	5071
2284	4966	2338	5020	2392	5072
2285	4967	2339	5021	2393	5073
2286	4968	2340	NONE	2394	5074
2287	4969	2341	5022	2395	5075
2288	4970	2342	5023	2396	5076
2289	4971	2343	5024	2397	5077
2290	4972	2344	5025	2398	5078
2291	4973	2345	5026	2399	5079
2292	4974	2346	5027	2400	5080
2293	4975	2347	5028	2401	5081
2294	4976	2348	5029	2402	5082
2295	4977	2349	5030	2403	5083
2296	4978	2350	5031	2404	5084
2297	4979	2351	5032	2405	5085
2298	4980	2352	5033	2406	5086
2299	4981	2353	5034	2407	5087
2300	4982	2354	5035	2408	5088
2301	4983	2355	5036	2409	5089
2302	4984	2356	5037	2410	5090
2303	4985	2357	5038	2411	5091
2304	4986	2358	5039	2412	5092
2305	4987	2359	5040	2413	5093
2306	4988	2360	5041	2414	5094
2307	4989	2361	5042	2415	5095
2308	4990	2362	5043	2416	5096
2309	4991	2363	5044	2417	5097
2310	4992	2364	5045	2418	5098

TABLE 2 (cont)

2419	5099	2473	5151	2527	5205
2420	5100	2474	5152	2528	5206
2421	5101	2475	5153	2529	5207
2422	5102	2476	5154	2530	5208
2423	5103	2477	5155	2531	5209
2424	5104	2478	5156	2532	5210
2425	5105	2479	5157	2533	5211
2426	5106	2480	5158	2534	5212
2427	5107	2481	5159	2535	5213
2428	5108	2482	5160	2536	5214
2429	5109	2483	5161	2537	5215
2430	5110	2484	5162	2538	5216
2431	5111	2485	5163	2539	5217
2432	5112	2486	5164	2540	5218
2433	5113	2487	5165	2541	5219
2434	5114	2488	5166	2542	5220
2435	5115	2489	5167	2543	5221
2436	5116	2490	5168	2544	5222
2437	5117	2491	5169	2545	5223
2438	5118	2492	5170	2546	5224
2439	5119	2493	5171	2547	5225
2440	5120	2494	5172	2548	5226
2441	5121	2495	5173	2549	5227
2442	5122	2496	5174	2550	5228
2443	NONE	2497	5175	2551	5229
2444	5123	2498	5176	2552	5230
2445	5124	2499	5177	2553	5231
2446	5125	2500	5178	2554	5232
2447	5126	2501	5179	2555	5233
2448	5127	2502	5180	2556	5234
2449	5128	2503	5181	2557	5235
2450	5129	2504	5182	2558	5236
2451	5130	2505	5183	2559	5237
2452	5131	2506	5184	2560	5238
2453	5132	2507	5185	2561	5239
2454	5133	2508	5186	2562	5240
2455	5134	2509	5187	2563	5241
2456	5135	2510	5188	2564	5242
2457	5136	2511	5189	2565	5243
2458	5137	2512	5190	2566	5244
2459	5138	2513	5191	2567	5245
2460	5139	2514	5192	2568	5246
2461	5140	2515	5193	2569	5247
2462	5141	2516	5194	2570	5248
2463	5142	2517	5195	2571	5249
2464	5143	2518	5196	2572	5250
2465	5144	2519	5197	2573	5251
2466	5145	2520	5198	2574	5252
2467	5146	2521	5199	2575	5253
2468	5147	2522	5200	2576	5254
2469	NONE	2523	5201	2577	5255
2470	5148	2524	5202	2578	5256
2471	5149	2525	5203	2579	5257
2472	5150	2526	5204	2580	5258

TABLE 2 (cont)

2581	5259	2635	5312	2689	5365
2582	5260	2636	5313	2690	5366
2583	5261	2637	5314	2691	5367
2584	5262	2638	5315	2692	5368
2585	5263	2639	5316	2693	5369
2586	5264	2640	5317	2694	5370
2587	5265	2641	5318	2695	5371
2588	5266	2642	5319	2696	5372
2589	5267	2643	5320	2697	5373
2590	5268	2644	5321	2698	5374
2591	5269	2645	5322	2699	5375
2592	5270	2646	5323	2700	5376
2593	5271	2647	5324	2701	5377
2594	5272	2648	5325	2702	5378
2595	5273	2649	5326	2703	5379
2596	5274	2650	5327		
2597	5275	2651	5328		
2598	5276	2652	5329		
2599	NONE	2653	5330		
2600	5277	2654	5331		
2601	5278	2655	5332		
2602	5279	2656	5333		
2603	5280	2657	5334		
2604	5281	2658	5335		
2605	5282	2659	5336		
2606	5283	2660	5337		
2607	5284	2661	5338		
2608	5285	2662	5339		
2609	5286	2663	5340		
2610	5287	2664	5341		
2611	5288	2665	5342		
2612	5289	2666	5343		
2613	5290	2667	5344		
2614	5291	2668	5345		
2615	5292	2669	5346		
2616	5293	2670	5347		
2617	5294	2671	5348		
2618	5295	2672	5349		
2619	5296	2673	5350		
2620	5297	2674	5351		
2621	5298	2675	5352		
2622	5299	2676	5353		
2623	5300	2677	5354		
2624	5301	2678	5355		
2625	5302	2679	5356		
2626	5303	2680	5357		
2627	5304	2681	NONE		
2628	5305	2682	5358		
2629	5306	2683	5359		
2630	5307	2684	5360		
2631	5308	2685	5361		
2632	5309	2686	5362		
2633	5310	2687	5363		
2634	5311	2688	5364		

TABLE 3

COLD RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:	SEQ ID NO:	AFFYMETRIX ID NO:	SEQ ID NO:	AFFYMETRIX ID NO:
1	11991_G_AT	50	12269_S_AT	98	12550_S_AT
2	11992_AT	51	12270_AT		17103_S_AT
3	11997_AT	52	12284_AT	99	12552_AT
4	11998_AT	53	12287_S_AT	100	12555_S_AT
5	12001_AT		17570_G_AT	101	12576_S_AT
6	12006_S_AT	54	12293_AT	102	12581_S_AT
7	12007_AT	55	12294_S_AT		16645_S_AT
8	12009_AT	56	12300_AT	103	12587_AT
9	12018_AT	57	12307_AT	104	12597_AT
10	12022_AT	58	12312_AT	105	12602_AT
11	12026_AT	59	12315_AT	106	12610_AT
12	12031_AT	60	12324_I_AT	107	12631_AT
13	12047_AT	61	12331_S_AT	108	12646_AT
14	12051_AT	62	12336_AT	109	12649_AT
15	12052_AT	63	12344_AT	110	12650_AT
16	12053_AT	64	12348_AT	111	12653_AT
17	12060_AT	65	12353_AT	112	12661_AT
18	12072_AT	66	12359_S_AT	113	12666_AT
19	12074_AT	67	12372_AT	114	12674_AT
20	12102_AT	68	12374_I_AT	115	12675_S_AT
21	12112_AT		12726_F_AT	116	12678_I_AT
22	12117_AT	69	12390_AT	117	12681_S_AT
23	12125_AT	70	12395_S_AT	118	12688_AT
24	12130_AT	71	12405_AT	119	12702_AT
25	12143_AT	72	12408_AT	120	12705_F_AT
26	12145_S_AT	73	12410_G_AT	121	12736_F_AT
27	12149_AT	74	12419_AT	122	12737_F_AT
28	12156_AT	75	12427_AT	123	12758_AT
29	12163_AT	76	12431_AT	124	12760_G_AT
30	12166_I_AT	77	12436_AT	125	12762_R_AT
31	12167_AT	78	12438_AT	126	12764_F_AT
32	12169_I_AT	79	12443_S_AT	127	12766_AT
33	12175_AT	80	12447_AT		15115_F_AT
34	12176_AT	81	12450_S_AT	128	12767_AT
35	12179_AT	82	12452_AT	129	12768_AT
36	12187_AT	83	12474_AT	130	12772_AT
	15920_I_AT	84	12477_AT	131	12773_AT
37	12195_AT	85	12491_AT	132	12776_AT
38	12196_AT	86	12497_AT	133	12788_AT
39	12198_AT	87	12500_S_AT	134	12793_AT
40	12200_AT	88	12503_AT	135	12794_AT
41	12202_AT	89	12515_AT	136	12802_AT
42	12214_G_AT	90	12516_S_AT	137	12809_G_AT
43	12219_AT	91	12523_AT	138	12812_AT
44	12224_AT	92	12526_AT	139	12815_AT
45	12226_AT	93	12527_AT	140	12816_AT
46	12233_AT	94	12532_AT	141	12818_AT
47	12240_AT	95	12534_G_AT	142	12824_S_AT
48	12253_G_AT	96	12544_AT	143	12828_S_AT
49	12256_AT	97	12549_S_AT	144	12842_S_AT

TABLE 3 (cont)

145	12846_S_AT	194	13086_R_AT	238	13285_S_AT
146	12858_AT	195	13087_AT	239	13288_S_AT
147	12860_S_AT	196	13090_AT		17043_S_AT
148	12861_S_AT	197	13092_S_AT	240	13292_S_AT
149	12881_S_AT		16950_S_AT	241	13296_S_AT
	17600_S_AT	198	13098_AT	242	13297_S_AT
150	12889_S_AT	199	13100_AT	243	13299_S_AT
151	12901_S_AT	200	13103_AT		15166_S_AT
152	12902_AT	201	13105_AT	244	13332_AT
153	12904_S_AT	202	13107_S_AT	245	13347_AT
154	12905_S_AT	203	13108_AT	246	13351_AT
155	12908_S_AT	204	13109_AT	247	13352_AT
156	12910_S_AT	205	13114_AT	248	13355_AT
	16385_S_AT	206	13118_F_AT	249	13404_AT
157	12914_S_AT	207	13119_AT	250	13422_AT
	15783_S_AT	208	13120_AT	251	13459_AT
	17645_S_AT	209	13123_AT	252	13460_AT
158	12916_S_AT	210	13128_AT	253	13461_S_AT
159	12923_S_AT	211	13133_S_AT	254	13467_AT
160	12926_S_AT		17430_S_AT	255	13488_AT
161	12927_S_AT	212	13135_S_AT	256	13523_S_AT
162	12931_S_AT	213	13139_AT	257	13529_AT
163	12937_R_AT	214	13140_AT	258	13539_I_AT
164	12941_G_AT	215	13143_AT		14631_S_AT
165	12942_AT	216	13151_G_AT	259	13541_AT
166	12947_AT	217	13160_AT	260	13542_AT
167	12949_AT	218	13161_AT	261	13545_S_AT
168	12953_AT	219	13162_AT	262	13552_AT
169	12956_I_AT	220	13165_AT	263	13556_I_AT
170	12959_AT	221	13166_AT	264	13561_AT
171	12966_S_AT	222	13167_AT	265	13563_S_AT
172	12975_AT	223	13179_AT	266	13567_AT
173	12983_AT	224	13181_AT	267	13568_AT
174	12984_AT	225	13185_AT	268	13571_AT
175	12987_S_AT	226	13193_S_AT	269	13575_AT
176	12994_S_AT	227	13213_S_AT	270	13576_AT
177	13002_AT		16004_S_AT	271	13583_AT
178	13009_I_AT	228	13219_S_AT	272	13598_AT
179	13011_AT		20288_G_AT	273	13601_AT
180	13018_AT	229	13220_S_AT	274	13604_AT
181	13023_AT		13221_AT	275	13613_AT
182	13024_AT		18929_S_AT	276	13616_S_AT
183	13034_S_AT	230	13233_AT		16544_S_AT
184	13046_G_AT		14301_S_AT	277	13617_AT
185	13048_S_AT	231	13243_R_AT	278	13618_S_AT
	13495_S_AT	232	13254_S_AT	279	13619_AT
186	13054_AT	233	13260_S_AT	280	13621_G_AT
187	13067_S_AT		15660_S_AT	281	13623_R_AT
188	13068_AT	234	13273_S_AT	282	13629_S_AT
189	13073_S_AT		16105_S_AT	283	13631_AT
190	13078_S_AT	235	13274_S_AT	284	13635_AT
191	13079_AT		17077_S_AT	285	13646_AT
192	13081_S_AT	236	13276_S_AT	286	13650_AT
193	13083_AT	237	13278_F_AT	287	13653_AT

TABLE 3 (cont)

288	13655_AT	332	13989_AT	383	14393_AT
289	13656_AT		20674_S_AT	384	14421_AT
290	13657_AT	333	14010_AT	385	14436_AT
291	13666_S_AT	334	14013_AT	386	14448_AT
	17083_S_AT	335	14014_AT	387	14450_AT
292	13667_S_AT	336	14019_AT	388	14454_AT
293	13669_S_AT	337	14021_R_AT	389	14459_AT
	17074_S_AT	338	14025_S_AT	390	14478_AT
294	13670_S_AT		18909_S_AT	391	14482_AT
	15206_S_AT	339	14027_AT	392	14485_AT
295	13671_S_AT	340	14030_AT	393	14492_S_AT
	16805_S_AT	341	14044_AT	394	14505_AT
296	13678_S_AT	342	14048_AT	395	14510_AT
297	13688_S_AT	343	14056_AT	396	14511_AT
298	13690_S_AT	344	14057_AT	397	14517_AT
	16065_S_AT	345	14058_AT	398	14519_AT
299	13691_S_AT	346	14059_AT	399	14525_S_AT
	16117_S_AT	347	14061_AT	400	14527_AT
300	13692_S_AT	348	14068_S_AT	401	14534_S_AT
	16118_S_AT	349	14072_AT	402	14538_R_AT
301	13700_AT	350	14073_AT	403	14554_AT
302	13704_S_AT	351	14074_AT	404	14558_AT
303	13714_AT	352	14084_AT	405	14559_S_AT
304	13715_AT	353	14095_S_AT	406	14566_AT
305	13724_AT	354	14100_AT	407	14572_AT
306	13748_AT	355	14101_AT	408	14579_AT
307	13759_AT	356	14103_AT	409	14587_AT
308	13767_AT	357	14105_AT	410	14591_AT
309	13785_AT	358	14106_AT	411	14595_AT
310	13803_AT	359	14121_AT	412	14602_AT
311	13850_I_AT	360	14129_S_AT	413	14603_AT
312	13876_AT	361	14133_S_AT	414	14605_AT
313	13880_S_AT	362	14143_AT	415	14620_S_AT
314	13883_AT	363	14145_AT	416	14626_S_AT
315	13887_S_AT	364	14148_AT	417	14630_S_AT
316	13895_AT	365	14186_AT		16559_S_AT
317	13904_S_AT	366	14194_AT	418	14637_S_AT
	18722_S_AT	367	14196_AT		17122_S_AT
318	13906_S_AT	368	14223_AT	419	14642_F_AT
319	13908_S_AT	369	14234_AT	420	14650_S_AT
	18597_AT	370	14236_AT		15150_S_AT
320	13923_AT	371	14251_F_AT	421	14654_S_AT
321	13927_AT	372	14252_F_AT	422	14667_S_AT
322	13932_AT	373	14270_AT		18299_S_AT
323	13935_AT	374	14298_G_AT	423	14669_S_AT
324	13940_AT		17581_G_AT		16136_S_AT
325	13949_S_AT	375	14303_S_AT	424	14672_S_AT
326	13954_G_AT	376	14312_AT	425	14679_S_AT
327	13971_S_AT	377	14316_AT	426	14682_I_AT
328	13973_AT	378	14339_AT	427	14689_AT
329	13983_AT	379	14366_AT	428	14697_G_AT
330	13985_S_AT	380	14369_AT		16902_AT
331	13987_S_AT	381	14388_AT	429	14701_S_AT
	18738_F_AT	382	14392_G_AT		14734_S_AT

TABLE 3 (cont)

430	14703_AT	483	15130_S_AT	534	15489_AT
431	14711_S_AT	484	15131_S_AT	535	15490_AT
432	14712_S_AT	485	15132_S_AT	536	15503_AT
	20530_S_AT		17585_S_AT	537	15505_AT
433	14713_S_AT	486	15139_S_AT	538	15510_R_AT
434	14715_S_AT	487	15143_S_AT	539	15512_AT
435	14728_S_AT	488	15146_S_AT	540	15514_AT
436	14731_S_AT	489	15159_S_AT	541	15515_R_AT
437	14781_AT		15160_S_AT	542	15517_S_AT
438	14797_S_AT	490	15162_S_AT	543	15518_AT
439	14800_AT	491	15167_S_AT	544	15529_AT
440	14809_AT	492	15171_S_AT	545	15534_F_AT
441	14843_AT	493	15174_F_AT	546	15538_AT
442	14847_AT	494	15178_S_AT	547	15541_AT
443	14872_AT	495	15185_S_AT	548	15543_AT
444	14886_AT		18023_S_AT	549	15544_AT
445	14896_AT	496	15188_S_AT	550	15551_AT
446	14900_AT	497	15193_S_AT	551	15574_S_AT
447	14908_AT	498	15196_S_AT	552	15576_S_AT
448	14912_AT	499	15197_S_AT	553	15577_S_AT
449	14914_AT	500	15201_F_AT	554	15578_S_AT
450	14942_AT	501	15213_S_AT	555	15583_S_AT
451	14945_AT	502	15243_AT	556	15588_S_AT
452	14955_AT	503	15256_AT	557	15595_S_AT
453	14957_S_AT	504	15270_AT	558	15600_S_AT
454	14958_AT	505	15319_AT	559	15602_F_AT
455	14965_AT	506	15325_AT	560	15608_S_AT
456	14974_AT	507	15337_AT	561	15613_S_AT
457	14980_AT	508	15341_AT	562	15616_S_AT
458	14981_AT	509	15343_AT	563	15618_S_AT
459	14984_S_AT	510	15348_AT	564	15620_S_AT
460	14995_AT	511	15350_AT	565	15627_S_AT
461	15004_AT	512	15355_S_AT	566	15634_S_AT
462	15009_AT	513	15367_AT		16125_S_AT
463	15010_AT	514	15372_AT		18046_S_AT
464	15024_AT	515	15379_AT	567	15637_S_AT
465	15026_AT	516	15381_AT	568	15639_S_AT
466	15036_R_AT	517	15383_AT	569	15642_S_AT
467	15054_AT	518	15384_AT	570	15643_S_AT
468	15056_AT	519	15385_AT	571	15651_F_AT
469	15057_AT	520	15387_AT	572	15652_S_AT
470	15066_AT	521	15410_AT	573	15665_S_AT
471	15073_AT	522	15417_S_AT	574	15667_S_AT
472	15081_AT	523	15422_AT		18610_S_AT
473	15083_AT	524	15423_AT	575	15668_S_AT
474	15091_AT	525	15431_AT	576	15671_S_AT
475	15097_S_AT	526	15433_AT	577	15675_S_AT
476	15101_S_AT	527	15452_AT	578	15679_S_AT
477	15102_S_AT	528	15464_AT	579	15685_S_AT
478	15107_S_AT	529	15468_AT	580	15687_F_AT
479	15112_S_AT	530	15471_AT	581	15688_S_AT
480	15116_F_AT	531	15472_AT	582	15689_S_AT
481	15118_S_AT	532	15475_S_AT	583	15692_S_AT
482	15122_S_AT	533	15485_AT	584	15694_S_AT

TABLE 3 (cont)

585	15712_S_AT	634	16089_S_AT	686	16496_S_AT
586	15808_AT	635	16090_S_AT	687	16499_AT
587	15845_AT	636	16102_S_AT	688	16510_AT
588	15848_AT	637	16103_S_AT	689	16511_AT
589	15850_AT	638	16108_S_AT	690	16512_S_AT
	20406_G_AT	639	16112_S_AT		18085_R_AT
590	15858_AT	640	16134_S_AT	691	16514_AT
591	15862_AT	641	16137_S_AT	692	16516_AT
592	15868_AT	642	16138_S_AT	693	16517_AT
593	15878_AT	643	16140_S_AT	694	16526_AT
594	15894_AT	644	16143_S_AT	695	16528_AT
595	15900_AT	645	16145_S_AT	696	16531_S_AT
596	15901_AT	646	16148_S_AT	697	16535_S_AT
597	15902_AT	647	16151_S_AT	698	16537_S_AT
598	15912_AT	648	16155_S_AT	699	16538_S_AT
599	15913_AT	649	16158_F_AT	700	16543_S_AT
600	15928_AT	650	16160_F_AT	701	16550_S_AT
601	15940_AT	651	16162_S_AT	702	16554_S_AT
602	15941_AT	652	16168_S_AT	703	16567_S_AT
603	15945_AT	653	16169_S_AT	704	16571_S_AT
604	15948_S_AT	654	16171_S_AT	705	16576_F_AT
605	15956_AT	655	16172_S_AT	706	16577_S_AT
606	15960_AT	656	16184_AT	707	16579_S_AT
	16466_S_AT	657	16192_AT	708	16580_S_AT
607	15976_AT	658	16222_AT	709	16583_S_AT
608	15978_AT	659	16242_AT	710	16584_S_AT
609	15986_S_AT	660	16244_AT		18706_S_AT
610	15990_AT	661	16250_AT	711	16593_S_AT
611	16009_S_AT	662	16286_AT	712	16595_S_AT
612	16015_AT	663	16288_AT	713	16598_S_AT
613	16019_AT	664	16294_S_AT	714	16604_S_AT
614	16024_AT	665	16296_AT	715	16605_S_AT
615	16034_AT	666	16297_AT	716	16610_S_AT
616	16036_I_AT	667	16325_AT	717	16611_S_AT
	18729_AT	668	16346_S_AT	718	16614_S_AT
617	16039_S_AT	669	16357_AT	719	16617_S_AT
618	16040_AT	670	16380_AT	720	16618_S_AT
619	16042_S_AT	671	16382_AT	721	16620_S_AT
620	16047_AT	672	16393_S_AT	722	16621_S_AT
621	16049_S_AT	673	16402_S_AT	723	16631_S_AT
622	16051_S_AT	674	16411_S_AT	724	16634_S_AT
623	16055_S_AT	675	16442_S_AT	725	16635_S_AT
624	16059_S_AT	676	16446_AT	726	16636_S_AT
625	16062_S_AT	677	16448_G_AT	727	16639_S_AT
626	16066_S_AT	678	16453_S_AT	728	16640_S_AT
627	16069_S_AT	679	16457_S_AT	729	16650_S_AT
628	16074_S_AT	680	16465_AT	730	16652_S_AT
629	16076_S_AT		16916_S_AT	731	16654_AT
630	16077_S_AT	681	16470_S_AT	732	16672_AT
	17579_S_AT		18735_S_AT	733	16673_AT
631	16079_S_AT	682	16481_S_AT	734	16687_S_AT
632	16084_S_AT	683	16486_AT	735	16747_AT
	17998_S_AT	684	16487_AT	736	16753_AT
633	16087_S_AT	685	16488_AT	737	16768_AT

TABLE 3 (cont)

738	16777_AT	790	17123_S_AT	843	17562_AT
739	16784_AT	791	17129_S_AT	844	17564_S_AT
740	16807_AT	792	17132_AT		19361_S_AT
741	16811_AT	793	17166_AT	845	17565_S_AT
742	16845_AT	794	17206_AT	846	17568_AT
743	16894_AT	795	17207_AT	847	17573_AT
744	16899_AT	796	17215_AT	848	17577_G_AT
745	16911_AT	797	17237_AT	849	17578_AT
746	16920_AT	798	17247_AT	850	17596_AT
747	16921_AT	799	17254_AT	851	17627_AT
748	16924_S_AT	800	17286_AT	852	17631_AT
749	16926_S_AT	801	17288_S_AT	853	17632_AT
750	16931_S_AT	802	17292_AT	854	17672_AT
751	16934_S_AT	803	17300_AT	855	17675_AT
752	16937_AT	804	17303_S_AT	856	17677_AT
753	16938_AT	805	17318_AT	857	17732_AT
754	16942_AT	806	17319_AT	858	17743_AT
755	16943_S_AT	807	17322_AT	859	17748_AT
	18231_AT	808	17323_AT	860	17782_AT
756	16949_S_AT	809	17332_S_AT	861	17823_S_AT
757	16952_S_AT	810	17374_AT	862	17841_AT
758	16956_AT	811	17381_AT	863	17849_S_AT
759	16962_S_AT	812	17388_AT	864	17852_G_AT
760	16965_S_AT	813	17392_S_AT	865	17857_AT
761	16970_S_AT	814	17405_AT	866	17865_AT
	18010_S_AT	815	17415_AT	867	17882_AT
762	16977_AT	816	17418_S_AT	868	17885_AT
763	16984_AT	817	17420_AT	869	17900_S_AT
764	16996_S_AT	818	17423_S_AT	870	17910_AT
765	16997_AT	819	17426_AT	871	17911_AT
766	17000_AT	820	17427_AT	872	17916_AT
767	17005_AT	821	17429_S_AT	873	17917_S_AT
768	17010_S_AT	822	17431_AT	874	17918_AT
769	17017_S_AT	823	17439_G_AT	875	17921_S_AT
770	17031_S_AT	824	17457_AT	876	17922_AT
771	17033_S_AT	825	17458_AT	877	17926_S_AT
772	17053_S_AT	826	17462_S_AT	878	17933_AT
773	17055_S_AT	827	17463_AT	879	17935_AT
774	17063_S_AT	828	17465_AT	880	17956_I_AT
775	17068_S_AT	829	17466_S_AT	881	17966_AT
776	17070_S_AT	830	17475_AT	882	17967_AT
777	17075_S_AT	831	17479_AT	883	17970_I_AT
778	17084_S_AT	832	17482_S_AT	884	17978_S_AT
779	17087_S_AT	833	17495_S_AT		20635_S_AT
780	17092_S_AT	834	17508_S_AT	885	17986_S_AT
781	17095_S_AT	835	17522_S_AT	886	17993_AT
782	17096_S_AT	836	17523_S_AT	887	18001_AT
783	17102_S_AT	837	17537_S_AT	888	18003_AT
784	17105_S_AT	838	17538_S_AT	889	18004_AT
785	17109_S_AT	839	17539_S_AT	890	18005_AT
786	17110_S_AT	840	17546_S_AT	891	18029_G_AT
787	17113_S_AT		18694_S_AT		18030_I_AT
788	17115_S_AT	841	17557_S_AT	892	18040_S_AT
789	17116_S_AT	842	17560_S_AT	893	18045_AT

TABLE 3 (cont)

894	18064_R_AT	947	18580_AT	1001	18889_AT
895	18065_R_AT	948	18581_AT	1002	18892_S_AT
896	18074_AT	949	18584_AT	1003	18901_AT
897	18076_S_AT	950	18587_S_AT	1004	18911_AT
898	18077_AT	951	18588_AT	1005	18917_I_AT
899	18081_AT	952	18591_AT	1006	18939_AT
900	18154_S_AT	953	18592_S_AT	1007	18947_I_AT
	18365_S_AT	954	18600_AT	1008	18950_AT
901	18165_AT	955	18601_S_AT	1009	18951_S_AT
902	18174_AT	956	18607_S_AT	1010	18954_AT
903	18176_AT	957	18611_AT	1011	18956_AT
904	18194_I_AT	958	18616_AT	1012	18959_AT
905	18197_AT	959	18622_G_AT	1013	18966_AT
906	18198_AT	960	18623_AT	1014	18974_AT
907	18213_AT	961	18628_AT	1015	18976_AT
908	18219_AT	962	18631_AT	1016	18980_AT
909	18221_AT	963	18635_AT	1017	18989_S_AT
910	18222_AT	964	18636_AT	1018	18994_AT
911	18226_S_AT	965	18638_AT	1019	19030_AT
912	18232_AT	966	18652_AT	1020	19039_AT
913	18237_AT	967	18657_AT	1021	19049_AT
914	18241_AT	968	18659_AT	1022	19083_AT
915	18257_AT	969	18660_S_AT	1023	19115_AT
916	18258_S_AT	970	18667_AT	1024	19117_S_AT
917	18269_S_AT	971	18675_AT	1025	19122_AT
918	18274_S_AT	972	18684_AT	1026	19125_S_AT
919	18275_AT	973	18686_S_AT	1027	19127_AT
920	18278_AT	974	18688_S_AT	1028	19130_AT
921	18282_AT	975	18693_S_AT	1029	19144_AT
922	18283_AT	976	18698_S_AT	1030	19157_S_AT
923	18290_AT	977	18705_AT	1031	19178_AT
924	18291_AT	978	18707_AT	1032	19190_G_AT
925	18306_AT	979	18708_AT	1033	19198_AT
926	18316_AT	980	18726_S_AT	1034	19202_AT
927	18317_AT	981	18727_AT	1035	19209_S_AT
928	18327_S_AT	982	18732_I_AT	1036	19211_AT
929	18337_S_AT	983	18736_AT	1037	19218_AT
930	18339_AT	984	18750_F_AT	1038	19222_AT
931	18347_S_AT	985	18754_AT	1039	19226_G_AT
932	18383_AT	986	18778_AT	1040	19229_AT
933	18390_AT	987	18806_S_AT	1041	19230_AT
934	18439_S_AT	988	18823_S_AT	1042	19232_S_AT
935	18465_S_AT	989	18829_AT	1043	19285_AT
936	18487_AT	990	18835_AT	1044	19326_AT
937	18508_S_AT	991	18844_AT	1045	19332_AT
938	18512_AT	992	18859_AT	1046	19346_AT
939	18543_AT	993	18864_AT	1047	19347_AT
940	18544_AT	994	18866_AT	1048	19362_AT
941	18552_AT	995	18880_AT	1049	19363_AT
942	18555_AT	996	18883_G_AT	1050	19364_AT
943	18556_AT	997	18885_AT	1051	19367_AT
944	18561_AT	998	18886_AT	1052	19373_AT
945	18567_AT	999	18887_AT	1053	19381_AT
946	18573_AT	1000	18888_AT	1054	19382_AT

TABLE 3 (cont)

1055	19384_AT	1109	19833_S_AT	1163	20093_I_AT
1056	19401_AT	1110	19834_AT	1164	20099_AT
1057	19406_AT	1111	19836_AT	1165	20100_AT
1058	19413_AT	1112	19841_AT	1166	20113_S_AT
1059	19416_AT	1113	19845_G_AT	1167	20117_AT
1060	19426_S_AT	1114	19854_AT	1168	20123_AT
1061	19439_AT	1115	19855_AT	1169	20127_S_AT
1062	19441_S_AT	1116	19866_AT	1170	20129_AT
1063	19442_AT	1117	19867_AT	1171	20150_AT
1064	19448_S_AT	1118	19870_S_AT	1172	20154_AT
1065	19454_AT	1119	19871_AT	1173	20156_AT
1066	19462_S_AT	1120	19872_AT	1174	20165_AT
1067	19464_AT	1121	19875_S_AT	1175	20173_AT
1068	19470_AT	1122	19876_AT	1176	20178_S_AT
1069	19483_AT	1123	19879_S_AT	1177	20183_AT
1070	19489_S_AT	1124	19881_AT	1178	20188_AT
1071	19513_AT	1125	19897_S_AT	1179	20189_AT
1072	19548_AT	1126	19903_AT	1180	20197_AT
1073	19562_AT	1127	19905_AT	1181	20210_G_AT
1074	19563_S_AT	1128	19906_AT	1182	20213_AT
1075	19567_AT	1129	19907_AT	1183	20229_AT
1076	19581_AT	1130	19910_AT	1184	20232_S_AT
1077	19589_S_AT	1131	19913_AT	1185	20255_AT
1078	19595_S_AT	1132	19920_S_AT	1186	20257_AT
1079	19606_AT	1133	19932_AT	1187	20262_AT
1080	19623_AT	1134	19939_AT	1188	20275_AT
1081	19624_AT	1135	19945_AT	1189	20278_S_AT
1082	19627_S_AT	1136	19947_AT	1190	20282_S_AT
1083	19636_AT	1137	19951_AT	1191	20284_AT
1084	19652_AT	1138	19956_AT	1192	20293_AT
1085	19655_AT	1139	19962_AT	1193	20294_AT
1086	19657_S_AT	1140	19963_AT	1194	20312_S_AT
1087	19658_AT	1141	19969_AT	1195	20315_I_AT
1088	19660_AT	1142	19970_S_AT	1196	20330_S_AT
1089	19665_S_AT	1143	19971_AT	1197	20331_AT
1090	19667_AT	1144	19972_AT	1198	20350_S_AT
1091	19671_AT	1145	19981_AT	1199	20354_S_AT
1092	19677_AT	1146	19990_AT	1200	20355_AT
1093	19686_AT	1147	19996_AT	1201	20360_AT
1094	19689_AT	1148	20003_S_AT	1202	20363_AT
1095	19690_S_AT	1149	20009_S_AT	1203	20369_S_AT
1096	19695_AT	1150	20013_AT	1204	20378_G_AT
1097	19698_AT	1151	20018_AT	1205	20383_AT
1098	19700_S_AT	1152	20024_S_AT	1206	20384_AT
1099	19708_AT	1153	20027_AT	1207	20387_AT
1100	19717_AT	1154	20045_AT	1208	20393_AT
1101	19726_S_AT	1155	20047_AT	1209	20396_AT
1102	19744_AT	1156	20048_AT	1210	20399_AT
1103	19752_S_AT	1157	20050_AT	1211	20409_G_AT
1104	19759_AT	1158	20051_AT	1212	20412_S_AT
1105	19782_AT	1159	20058_AT	1213	20413_AT
1106	19803_S_AT	1160	20067_AT	1214	20439_AT
1107	19828_AT	1161	20068_AT	1215	20440_AT
1108	19831_I_AT	1162	20069_AT	1216	20444_AT

TABLE 3 (cont)

1217	20445_AT
1218	20449_AT
1219	20456_AT
1220	20462_AT
1221	20471_AT
1222	20474_AT
1223	20495_S_AT
1224	20499_AT
1225	20501_AT
1226	20511_AT
1227	20515_S_AT
1228	20516_AT
1229	20517_AT
1230	20518_AT
1231	20520_S_AT
1232	20536_S_AT
1233	20538_S_AT
1234	20539_S_AT
1235	20558_AT
1236	20561_AT
1237	20567_AT
1238	20571_AT
1239	20582_S_AT
1240	20586_I_AT
1241	20590_AT
1242	20592_AT
1243	20594_AT
1244	20608_S_AT
1245	20612_S_AT
1246	20616_AT
1247	20620_G_AT
1248	20637_AT
1249	20643_AT
1250	20649_AT
1251	20651_AT
1252	20654_S_AT
1253	20670_AT
1254	20684_AT
1255	20685_AT
1256	20693_AT
1257	20701_S_AT
1258	20704_AT
1259	20705_AT
1260	20715_AT
1261	20719_AT

TABLE 4: 2X UP IN COLD, ONLY

11997_at	12688_at	13274_s_at	14145_at	15083_at	15639_s_at
11998_at	12701_i_at	13278_f_at	14170_at	15084_at	15641_s_at
12018_at	12702_at	13279_s_at	14186_at	15096_at	15660_s_at
12031_at	12719_f_at	13285_s_at	14196_at	15101_s_at	15665_s_at
12047_at	12726_f_at	13288_s_at	14227_at	15105_s_at	15687_f_at
12051_at	12736_f_at	13292_s_at	14234_at	15112_s_at	15694_s_at
12053_at	12754_g_at	13297_s_at	14250_r_at	15115_f_at	15712_s_at
12060_at	12762_r_at	13299_s_at	14270_at	15116_f_at	15783_s_at
12072_at	12766_at	13332_at	14298_g_at	15122_s_at	15808_at
12074_at	12767_at	13351_at	14303_s_at	15126_s_at	15837_at
12102_at	12768_at	13352_at	14312_at	15131_s_at	15850_at
12112_at	12773_at	13422_at	14339_at	15132_s_at	15862_at
12117_at	12788_at	13435_at	14388_at	15137_s_at	15868_at
12130_at	12802_at	13461_s_at	14393_at	15144_s_at	15878_at
12145_s_at	12860_s_at	13467_at	14511_at	15148_s_at	15901_at
12151_at	12861_s_at	13488_at	14525_s_at	15153_s_at	15912_at
12163_at	12879_s_at	13495_s_at	14527_at	15159_s_at	15920_i_at
12175_at	12891_at	13539_i_at	14534_s_at	15160_s_at	15941_at
12187_at	12914_s_at	13542_at	14554_at	15166_s_at	15945_at
12195_at	12927_s_at	13575_at	14566_at	15174_f_at	15960_at
12219_at	12947_at	13577_s_at	14579_at	15197_s_at	15990_at
12256_at	12956_i_at	13617_at	14591_at	15270_at	16001_at
12269_s_at	12966_s_at	13634_s_at	14595_at	15319_at	16009_s_at
12307_at	12974_at	13656_at	14600_at	15325_at	16010_s_at
12315_at	12987_s_at	13671_s_at	14631_s_at	15337_at	16034_at
12336_at	12994_s_at	13691_s_at	14635_s_at	15341_at	16036_i_at
12349_s_at	12998_at	13700_at	14679_s_at	15343_at	16039_s_at
12353_at	13002_at	13704_s_at	14691_at	15355_s_at	16040_at
12359_s_at	13018_at	13709_s_at	14697_g_at	15367_at	16042_s_at
12390_at	13023_at	13715_at	14709_at	15379_at	16047_at
12395_s_at	13046_g_at	13785_at	14711_s_at	15381_at	16049_s_at
12431_at	13054_at	13803_at	14728_s_at	15410_at	16051_s_at
12436_at	13086_r_at	13812_s_at	14731_s_at	15417_s_at	16062_s_at
12443_s_at	13087_at	13825_s_at	14797_s_at	15422_at	16079_s_at
12447_at	13100_at	13850_i_at	14809_at	15433_at	16087_s_at
12452_at	13109_at	13904_s_at	14843_at	15451_at	16090_s_at
12477_at	13119_at	13908_s_at	14847_at	15452_at	16117_s_at
12503_at	13120_at	13927_at	14872_at	15453_s_at	16118_s_at
12516_s_at	13128_at	13971_s_at	14886_at	15472_at	16137_s_at
12532_at	13134_s_at	13985_s_at	14896_at	15489_at	16155_s_at
12544_at	13140_at	14013_at	14897_at	15490_at	16162_s_at
12561_at	13143_at	14019_at	14900_at	15503_at	16184_at
12602_at	13167_at	14021_r_at	14956_s_at	15510_r_at	16192_at
12610_at	13172_s_at	14028_at	14958_at	15517_s_at	16222_at
12631_at	13178_at	14048_at	14965_at	15518_at	16244_at
12647_s_at	13179_at	14058_at	14984_s_at	15544_at	16250_at
12650_at	13181_at	14059_at	15004_at	15588_s_at	16260_at
12656_at	13187_i_at	14064_at	15010_at	15600_s_at	16286_at
12674_at	13209_s_at	14073_at	15036_r_at	15605_s_at	16296_at
12675_s_at	13219_s_at	14105_at	15040_g_at	15613_s_at	16297_at
12676_s_at	13221_at	14106_at	15046_s_at	15614_s_at	16342_at
12681_s_at	13243_r_at	14126_s_at	15057_at	15616_s_at	16367_i_at
12686_s_at	13260_s_at	14140_at	15073_at	15633_s_at	16411_s_at

TABLE 4 (cont): 2X UP IN COLD, ONLY

16442_s_at	17077_s_at	17978_s_at	18885_at	19689_at	20412_s_at
16465_at	17102_s_at	17999_at	18887_at	19698_at	20413_at
16466_s_at	17109_s_at	18001_at	18888_at	19700_s_at	20432_at
16468_at	17113_s_at	18004_at	18889_at	19707_s_at	20433_at
16486_at	17123_s_at	18012_s_at	18901_at	19708_at	20456_at
16487_at	17128_s_at	18040_s_at	18907_s_at	19713_at	20462_at
16488_at	17129_s_at	18176_at	18917_i_at	19718_at	20471_at
16489_at	17132_at	18194_i_at	18939_at	19744_at	20511_at
16496_s_at	17166_at	18197_at	18947_i_at	19836_at	20515_s_at
16499_at	17206_at	18198_at	18949_at	19839_at	20517_at
16511_at	17237_at	18213_at	18954_at	19840_s_at	20518_at
16517_at	17300_at	18219_at	18959_at	19845_g_at	20529_at
16538_s_at	17319_at	18222_at	18974_at	19854_at	20536_s_at
16554_s_at	17322_at	18231_at	18976_at	19855_at	20538_s_at
16571_s_at	17332_s_at	18232_at	18980_at	19860_at	20539_s_at
16576_f_at	17381_at	18241_at	18989_s_at	19866_at	20576_at
16595_s_at	17388_at	18269_s_at	19019_i_at	19871_at	20582_s_at
16605_s_at	17392_s_at	18272_at	19049_at	19875_s_at	20586_i_at
16610_s_at	17408_at	18282_at	19083_at	19879_s_at	20608_s_at
16620_s_at	17424_at	18298_at	19130_at	19881_at	20649_at
16621_s_at	17429_s_at	18316_at	19156_s_at	19913_at	20651_at
16635_s_at	17457_at	18317_at	19178_at	19939_at	20684_at
16636_s_at	17458_at	18331_s_at	19190_g_at	19945_at	20685_at
16638_s_at	17466_s_at	18347_s_at	19199_at	19947_at	20699_at
16650_s_at	17477_s_at	18383_at	19202_at	19951_at	20705_at
16672_at	17482_s_at	18390_at	19209_s_at	19956_at	20715_at
16673_at	17538_s_at	18455_at	19211_at	19971_at	
16687_s_at	17546_s_at	18465_s_at	19218_at	19976_at	
16747_at	17562_at	18544_at	19229_at	19998_at	
16753_at	17581_g_at	18555_at	19322_at	20003_s_at	
16768_at	17627_at	18556_at	19326_at	20015_at	
16805_s_at	17631_at	18560_at	19359_s_at	20027_at	
16807_at	17632_at	18561_at	19367_at	20051_at	
16845_at	17645_s_at	18571_at	19384_at	20068_at	
16847_at	17672_at	18588_at	19389_at	20093_i_at	
16896_s_at	17675_at	18597_at	19397_at	20117_at	
16899_at	17677_at	18601_s_at	19406_at	20150_at	
16902_at	17693_at	18611_at	19426_s_at	20156_at	
16911_at	17732_at	18623_at	19441_s_at	20165_at	
16914_s_at	17743_at	18635_at	19442_at	20257_at	
16943_s_at	17748_at	18659_at	19470_at	20262_at	
16956_at	17775_at	18660_s_at	19489_s_at	20275_at	
16996_s_at	17782_at	18673_at	19562_at	20282_s_at	
17010_s_at	17841_at	18694_s_at	19577_at	20288_g_at	
17016_s_at	17852_g_at	18705_at	19589_s_at	20293_at	
17032_s_at	17900_s_at	18708_at	19597_s_at	20315_i_at	
17033_s_at	17901_at	18738_f_at	19611_s_at	20330_s_at	
17043_s_at	17911_at	18750_f_at	19624_at	20360_at	
17050_s_at	17921_s_at	18778_at	19657_s_at	20363_at	
17055_s_at	17922_at	18829_at	19667_at	20369_s_at	
17068_s_at	17933_at	18835_at	19671_at	20384_at	
17071_s_at	17967_at	18866_at	19677_at	20393_at	
17075_s_at	17970_i_at	18875_s_at	19686_at	20396_at	

TABLE 5: 2X UP COLD 3 HR, ONLY

12117_at	13671_s_at	15453_s_at	17237_at	19624_at
12145_s_at	13691_s_at	15489_at	17319_at	19657_s_at
12151_at	13785_at	15518_at	17392_s_at	19667_at
12163_at	13803_at	15588_s_at	17429_s_at	19845_g_at
12187_at	13825_s_at	15613_s_at	17477_s_at	19855_at
12256_at	13904_s_at	15614_s_at	17538_s_at	19866_at
12315_at	14013_at	15616_s_at	17581_g_at	19945_at
12349_s_at	14021_r_at	15639_s_at	17627_at	19951_at
12353_at	14028_at	15641_s_at	17672_at	19998_at
12359_s_at	14064_at	15660_s_at	17693_at	20003_s_at
12544_at	14126_s_at	15687_f_at	17782_at	20015_at
12602_at	14145_at	15694_s_at	17841_at	20051_at
12610_at	14170_at	15862_at	17900_s_at	20093_i_at
12676_s_at	14196_at	15868_at	17933_at	20117_at
12686_s_at	14250_r_at	15878_at	17978_s_at	20288_g_at
12701_i_at	14298_g_at	15901_at	18001_at	20360_at
12702_at	14303_s_at	16034_at	18012_s_at	20369_s_at
12719_f_at	14339_at	16039_s_at	18198_at	20384_at
12736_f_at	14527_at	16040_at	18219_at	20462_at
12754_g_at	14534_s_at	16042_s_at	18241_at	20471_at
12766_at	14554_at	16047_at	18269_s_at	20515_s_at
12767_at	14595_at	16062_s_at	18272_at	20538_s_at
12768_at	14635_s_at	16087_s_at	18282_at	20576_at
12773_at	14679_s_at	16117_s_at	18298_at	20608_s_at
12788_at	14691_at	16118_s_at	18383_at	20651_at
12879_s_at	14697_g_at	16162_s_at	18556_at	20685_at
12891_at	14709_at	16184_at	18588_at	20705_at
12947_at	14728_s_at	16222_at	18601_s_at	
12966_s_at	14809_at	16250_at	18611_at	
12974_at	14896_at	16411_s_at	18694_s_at	
12994_s_at	14965_at	16442_s_at	18708_at	
13002_at	14984_s_at	16465_at	18738_f_at	
13100_at	15046_s_at	16486_at	18778_at	
13140_at	15083_at	16488_at	18829_at	
13167_at	15096_at	16489_at	18835_at	
13172_s_at	15105_s_at	16517_at	18866_at	
13179_at	15115_f_at	16571_s_at	18875_s_at	
13187_i_at	15116_f_at	16605_s_at	18888_at	
13219_s_at	15122_s_at	16610_s_at	18907_s_at	
13260_s_at	15126_s_at	16620_s_at	18917_i_at	
13278_f_at	15131_s_at	16636_s_at	18939_at	
13279_s_at	15132_s_at	16650_s_at	18974_at	
13285_s_at	15137_s_at	16805_s_at	19190_g_at	
13288_s_at	15153_s_at	16845_at	19199_at	
13292_s_at	15159_s_at	16899_at	19202_at	
13297_s_at	15160_s_at	16914_s_at	19211_at	
13351_at	15197_s_at	16943_s_at	19384_at	
13352_at	15355_s_at	16996_s_at	19406_at	
13435_at	15379_at	17010_s_at	19426_s_at	
13467_at	15417_s_at	17043_s_at	19442_at	
13488_at	15422_at	17068_s_at	19470_at	
13495_s_at	15451_at	17109_s_at	19577_at	
13656_at	15452_at	17128_s_at	19597_s_at	

TABLE 6: 2X DOWN COLD, ONLY

11991_g_at	12450_s_at	12881_s_at	13151_g_at	13621_g_at	14056_at
11992_at	12474_at	12889_s_at	13160_at	13623_r_at	14057_at
12001_at	12491_at	12901_s_at	13161_at	13629_s_at	14061_at
12006_s_at	12497_at	12902_at	13162_at	13631_at	14067_at
12007_at	12500_s_at	12904_s_at	13165_at	13635_at	14068_s_at
12009_at	12515_at	12905_s_at	13166_at	13646_at	14072_at
12022_at	12521_at	12908_s_at	13185_at	13650_at	14074_at
12023_s_at	12523_at	12910_s_at	13193_s_at	13652_at	14075_at
12026_at	12526_at	12916_s_at	13211_s_at	13653_at	14083_at
12037_at	12527_at	12923_s_at	13213_s_at	13655_at	14084_at
12052_at	12534_g_at	12926_s_at	13219_s_at	13657_at	14089_at
12125_at	12549_s_at	12931_s_at	13233_at	13666_s_at	14095_s_at
12143_at	12550_s_at	12937_r_at	13236_s_at	13667_s_at	14096_at
12149_at	12552_at	12941_g_at	13239_s_at	13669_s_at	14100_at
12156_at	12555_s_at	12942_at	13241_s_at	13670_s_at	14101_at
12166_i_at	12556_at	12949_at	13254_s_at	13672_s_at	14103_at
12167_at	12575_s_at	12953_at	13266_s_at	13678_s_at	14121_at
12169_i_at	12576_s_at	12958_at	13273_s_at	13679_s_at	14129_s_at
12176_at	12581_s_at	12959_at	13275_f_at	13688_s_at	14133_s_at
12179_at	12587_at	12966_s_at	13276_s_at	13690_s_at	14143_at
12196_at	12597_at	12975_at	13278_f_at	13691_s_at	14148_at
12198_at	12606_at	12983_at	13280_s_at	13692_s_at	14162_at
12200_at	12609_at	12984_at	13285_s_at	13714_at	14194_at
12202_at	12646_at	13002_at	13296_s_at	13724_at	14208_at
12212_at	12649_at	13009_i_at	13347_at	13748_at	14217_at
12214_g_at	12653_at	13011_at	13355_at	13751_at	14223_at
12224_at	12661_at	13014_at	13361_at	13759_at	14235_at
12226_at	12666_at	13024_at	13404_at	13767_at	14236_at
12233_at	12678_i_at	13034_s_at	13406_at	13789_at	14251_f_at
12240_at	12705_f_at	13041_s_at	13459_at	13876_at	14252_f_at
12253_g_at	12736_f_at	13048_s_at	13460_at	13880_s_at	14285_at
12270_at	12737_f_at	13067_s_at	13464_at	13883_at	14301_s_at
12278_at	12758_at	13068_at	13523_s_at	13887_s_at	14316_at
12284_at	12760_g_at	13073_s_at	13529_at	13895_at	14366_at
12287_s_at	12764_f_at	13078_s_at	13541_at	13906_s_at	14369_at
12293_at	12765_at	13079_at	13545_s_at	13919_at	14392_g_at
12294_s_at	12772_at	13081_s_at	13550_at	13923_at	14421_at
12300_at	12776_at	13083_at	13552_at	13932_at	14431_at
12312_at	12784_at	13090_at	13556_i_at	13935_at	14436_at
12315_at	12793_at	13092_s_at	13561_at	13940_at	14448_at
12324_i_at	12794_at	13098_at	13563_s_at	13949_s_at	14450_at
12331_s_at	12795_at	13103_at	13567_at	13954_g_at	14454_at
12344_at	12809_g_at	13105_at	13568_at	13973_at	14459_at
12348_at	12812_at	13107_s_at	13571_at	13983_at	14478_at
12353_at	12815_at	13108_at	13576_at	13989_at	14482_at
12372_at	12816_at	13114_at	13583_at	14010_at	14485_at
12374_i_at	12818_at	13118_f_at	13598_at	14014_at	14492_s_at
12405_at	12824_s_at	13123_at	13601_at	14015_s_at	14505_at
12408_at	12828_s_at	13124_at	13604_at	14016_s_at	14510_at
12410_g_at	12842_s_at	13133_s_at	13613_at	14025_s_at	14517_at
12419_at	12846_s_at	13135_s_at	13616_s_at	14027_at	14519_at
12427_at	12858_at	13139_at	13618_s_at	14030_at	14534_s_at
12438_at	12869_s_at	13146_s_at	13619_at	14044_at	14538_r_at

TABLE 6 (cont): 2X DOWN COLD, ONLY

14558_at	15047_at	15512_at	15940_at	16357_at	16894_at
14559_s_at	15054_at	15514_at	15948_s_at	16380_at	16899_at
14572_at	15056_at	15515_r_at	15956_at	16382_at	16920_at
14584_at	15058_s_at	15529_at	15976_at	16385_s_at	16921_at
14587_at	15063_at	15534_f_at	15978_at	16393_s_at	16924_s_at
14595_at	15066_at	15538_at	15986_s_at	16402_s_at	16926_s_at
14602_at	15081_at	15541_at	16004_s_at	16417_s_at	16931_s_at
14603_at	15091_at	15543_at	16015_at	16442_s_at	16934_s_at
14605_at	15097_s_at	15551_at	16017_at	16446_at	16937_at
14620_s_at	15102_s_at	15574_s_at	16019_at	16448_g_at	16938_at
14626_s_at	15107_s_at	15576_s_at	16024_at	16453_s_at	16942_at
14630_s_at	15118_s_at	15577_s_at	16031_at	16457_s_at	16949_s_at
14637_s_at	15127_s_at	15578_s_at	16055_s_at	16470_s_at	16950_s_at
14640_s_at	15130_s_at	15581_s_at	16059_s_at	16481_s_at	16952_s_at
14642_f_at	15132_s_at	15583_s_at	16065_s_at	16510_at	16962_s_at
14650_s_at	15133_s_at	15591_s_at	16066_s_at	16512_s_at	16965_s_at
14654_s_at	15139_s_at	15595_s_at	16069_s_at	16514_at	16970_s_at
14667_s_at	15143_s_at	15602_f_at	16074_s_at	16516_at	16977_at
14668_s_at	15146_s_at	15606_s_at	16076_s_at	16523_s_at	16984_at
14669_s_at	15150_s_at	15608_s_at	16077_s_at	16526_at	16989_at
14672_s_at	15161_s_at	15616_s_at	16084_s_at	16528_at	16993_at
14673_s_at	15162_s_at	15618_s_at	16089_s_at	16531_s_at	16997_at
14675_s_at	15167_s_at	15620_s_at	16102_s_at	16535_s_at	17000_at
14679_s_at	15170_s_at	15627_s_at	16103_s_at	16537_s_at	17005_at
14681_g_at	15171_s_at	15634_s_at	16105_s_at	16543_s_at	17010_s_at
14682_i_at	15178_s_at	15637_s_at	16108_s_at	16544_s_at	17017_s_at
14689_at	15182_s_at	15642_s_at	16112_s_at	16550_s_at	17031_s_at
14701_s_at	15185_s_at	15643_s_at	16117_s_at	16559_s_at	17040_s_at
14703_at	15188_s_at	15646_s_at	16118_s_at	16567_s_at	17053_s_at
14712_s_at	15193_s_at	15651_f_at	16125_s_at	16577_s_at	17056_s_at
14713_s_at	15196_s_at	15652_s_at	16127_s_at	16579_s_at	17063_s_at
14715_s_at	15201_f_at	15667_s_at	16134_s_at	16580_s_at	17070_s_at
14734_s_at	15206_s_at	15668_s_at	16136_s_at	16583_s_at	17074_s_at
14781_at	15207_s_at	15670_s_at	16138_s_at	16584_s_at	17084_s_at
14800_at	15213_s_at	15671_s_at	16140_s_at	16593_s_at	17085_s_at
14856_s_at	15243_at	15675_s_at	16143_s_at	16598_s_at	17087_s_at
14882_at	15256_at	15679_s_at	16144_s_at	16603_s_at	17092_s_at
14908_at	15348_at	15685_s_at	16145_s_at	16604_s_at	17095_s_at
14912_at	15350_at	15688_s_at	16148_s_at	16611_s_at	17096_s_at
14914_at	15372_at	15689_s_at	16151_s_at	16614_s_at	17097_s_at
14924_at	15383_at	15692_s_at	16158_f_at	16617_s_at	17103_s_at
14942_at	15384_at	15775_at	16160_f_at	16618_s_at	17105_s_at
14945_at	15385_at	15776_at	16168_s_at	16620_s_at	17110_s_at
14955_at	15387_at	15845_at	16169_s_at	16631_s_at	17115_s_at
14957_s_at	15406_at	15848_at	16171_s_at	16634_s_at	17116_s_at
14974_at	15423_at	15858_at	16172_s_at	16639_s_at	17119_s_at
14980_at	15431_at	15866_s_at	16222_at	16640_s_at	17122_s_at
14981_at	15464_at	15894_at	16232_s_at	16652_s_at	17207_at
14995_at	15468_at	15900_at	16242_at	16654_at	17215_at
15009_at	15471_at	15901_at	16288_at	16777_at	17247_at
15018_at	15475_s_at	15902_at	16294_s_at	16784_at	17254_at
15024_at	15485_at	15913_at	16325_at	16811_at	17286_at
15026_at	15505_at	15928_at	16346_s_at	16893_at	17288_s_at

TABLE 6 (cont): 2X DOWN COLD, ONLY

17292_at	17910_at	18337_s_at	18823_s_at	19382_at	19897_s_at
17303_s_at	17916_at	18339_at	18844_at	19401_at	19903_at
17305_at	17917_s_at	18365_s_at	18859_at	19402_at	19905_at
17318_at	17918_at	18402_at	18864_at	19406_at	19906_at
17323_at	17926_s_at	18439_s_at	18880_at	19413_at	19907_at
17374_at	17935_at	18487_at	18883_g_at	19416_at	19910_at
17405_at	17956_i_at	18508_s_at	18886_at	19429_at	19920_s_at
17415_at	17961_at	18512_at	18892_s_at	19432_s_at	19932_at
17418_s_at	17966_at	18543_at	18909_s_at	19439_at	19951_at
17420_at	17978_s_at	18552_at	18911_at	19448_s_at	19962_at
17423_s_at	17986_s_at	18567_at	18913_s_at	19454_at	19963_at
17426_at	17993_at	18573_at	18916_s_at	19462_s_at	19969_at
17427_at	17998_s_at	18580_at	18921_g_at	19464_at	19970_s_at
17430_s_at	18003_at	18581_at	18950_at	19469_at	19972_at
17431_at	18005_at	18584_at	18951_s_at	19483_at	19981_at
17439_g_at	18010_s_at	18587_s_at	18956_at	19484_s_at	19990_at
17442_i_at	18013_r_at	18590_at	18966_at	19513_at	19996_at
17449_s_at	18023_s_at	18591_at	18972_at	19548_at	19999_s_at
17462_s_at	18029_g_at	18592_s_at	18994_at	19563_s_at	20009_s_at
17463_at	18030_i_at	18600_at	19030_at	19567_at	20013_at
17465_at	18045_at	18601_s_at	19039_at	19581_at	20017_at
17475_at	18046_s_at	18607_s_at	19068_i_at	19595_s_at	20018_at
17479_at	18059_i_at	18610_s_at	19108_at	19606_at	20024_s_at
17495_s_at	18064_r_at	18611_at	19115_at	19623_at	20045_at
17508_s_at	18065_r_at	18616_at	19117_s_at	19627_s_at	20047_at
17522_s_at	18074_at	18622_g_at	19122_at	19636_at	20048_at
17523_s_at	18076_s_at	18628_at	19125_s_at	19641_at	20050_at
17529_s_at	18077_at	18631_at	19127_at	19652_at	20051_at
17537_s_at	18078_at	18636_at	19135_at	19655_at	20058_at
17539_s_at	18081_at	18638_at	19144_at	19658_at	20067_at
17543_s_at	18083_r_at	18652_at	19157_s_at	19660_at	20069_at
17555_s_at	18085_r_at	18657_at	19158_at	19665_s_at	20099_at
17557_s_at	18091_at	18667_at	19177_at	19667_at	20100_at
17560_s_at	18154_s_at	18675_at	19192_at	19690_s_at	20113_s_at
17564_s_at	18165_at	18684_at	19198_at	19695_at	20123_at
17565_s_at	18174_at	18686_s_at	19222_at	19717_at	20127_s_at
17568_at	18221_at	18688_s_at	19226_g_at	19726_s_at	20129_at
17570_g_at	18226_s_at	18693_s_at	19227_at	19752_s_at	20133_i_at
17573_at	18230_at	18698_s_at	19230_at	19759_at	20152_at
17577_g_at	18237_at	18706_s_at	19232_s_at	19782_at	20154_at
17578_at	18255_at	18707_at	19263_at	19789_s_at	20173_at
17579_s_at	18257_at	18726_s_at	19285_at	19803_s_at	20178_s_at
17585_s_at	18258_s_at	18727_at	19332_at	19828_at	20183_at
17596_at	18274_s_at	18732_i_at	19346_at	19831_i_at	20188_at
17600_s_at	18275_at	18735_s_at	19347_at	19833_s_at	20189_at
17823_s_at	18278_at	18736_at	19361_s_at	19834_at	20197_at
17840_s_at	18283_at	18738_f_at	19362_at	19835_at	20200_at
17849_s_at	18290_at	18747_f_at	19363_at	19841_at	20210_g_at
17857_at	18291_at	18754_at	19364_at	19867_at	20213_at
17865_at	18299_s_at	18782_at	19365_s_at	19870_s_at	20229_at
17882_at	18300_at	18789_at	19373_at	19871_at	20232_s_at
17885_at	18306_at	18806_s_at	19379_at	19872_at	20255_at
17902_s_at	18327_s_at	18814_at	19381_at	19876_at	20278_s_at

TABLE 6 (cont): 2X DOWN COLD, ONLY

20284_at	20693_at
20288_g_at	20701_s_at
20294_at	20704_at
20312_s_at	20707_s_at
20331_at	20719_at
20335_s_at	
20350_s_at	
20354_s_at	
20355_at	
20369_s_at	
20378_g_at	
20383_at	
20385_s_at	
20387_at	
20399_at	
20409_g_at	
20420_at	
20429_s_at	
20439_at	
20440_at	
20444_at	
20445_at	
20449_at	
20474_at	
20480_s_at	
20495_s_at	
20499_at	
20501_at	
20516_at	
20520_s_at	
20530_s_at	
20538_s_at	
20547_at	
20558_at	
20561_at	
20567_at	
20571_at	
20590_at	
20592_at	
20594_at	
20608_s_at	
20612_s_at	
20616_at	
20620_g_at	
20635_s_at	
20637_at	
20643_at	
20654_s_at	
20670_at	
20674_s_at	
20684_at	
20685_at	
20689_s_at	

TABLE 7

SALINE STRESS RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:	SEQ ID NO:	AFFYMETRIX ID NO:	SEQ ID NO:	AFFYMETRIX ID NO:
2227	12011_S_AT	2275	13993_S_AT	2324	15965_AT
2228	12153_AT	2276	14000_AT	2325	15969_S_AT
2229	12180_AT	2277	14003_AT	2326	15975_S_AT
2230	12186_AT	2278	14032_AT	2327	15995_S_AT
2231	12216_AT	2279	14043_AT	2328	15998_S_AT
2232	12265_AT	2280	14070_AT		18090_S_AT
2233	12335_AT	2281	14267_AT	2329	16028_AT
2234	12449_S_AT	2282	14269_AT	2330	16050_AT
2235	12470_AT	2283	14418_AT	2331	16060_S_AT
2236	12479_AT	2284	14427_AT	2332	16067_S_AT
2237	12487_AT	2285	14501_AT	2333	16072_S_AT
2238	12493_G_AT	2286	14544_AT	2334	16088_F_AT
2239	12562_AT	2287	14546_S_AT	2335	16273_AT
2240	12685_AT	2288	14570_AT	2336	16314_AT
2241	12704_F_AT	2289	14596_AT	2337	16413_S_AT
2242	12709_F_AT	2290	14729_S_AT	2338	16414_AT
2243	12734_F_AT	2291	14874_AT	2339	16426_AT
2244	12739_S_AT	2292	14888_AT	2340	16436_AT
2245	12750_S_AT	2293	14951_AT	2341	16455_AT
2246	12761_S_AT	2294	14952_AT	2342	16502_AT
2247	12813_AT	2295	14959_AT	2343	16548_S_AT
2248	12845_S_AT	2296	14979_AT	2344	16568_S_AT
2249	12946_AT	2297	15006_AT	2345	16582_S_AT
2250	13003_S_AT	2298	15042_AT	2346	16589_S_AT
2251	13052_S_AT	2299	15049_AT	2347	16594_S_AT
2252	13094_AT	2300	15062_AT	2348	16613_S_AT
2253	13142_AT	2301	15108_S_AT	2349	16651_S_AT
2254	13172_S_AT	2302	15147_S_AT	2350	16668_AT
	17880_S_AT	2303	15175_S_AT	2351	16820_AT
2255	13198_I_AT	2304	15176_S_AT	2352	16987_S_AT
2256	13209_S_AT	2305	15186_S_AT	2353	16995_AT
	16165_S_AT		18696_S_AT	2354	17039_S_AT
2257	13229_S_AT	2306	15192_S_AT	2355	17273_AT
2258	13253_F_AT	2307	15208_S_AT	2356	17278_AT
2259	13344_S_AT	2308	15324_AT	2357	17433_AT
2260	13370_AT	2309	15371_AT	2358	17467_AT
2261	13387_AT	2310	15424_AT	2359	17566_AT
2262	13408_S_AT	2311	15463_AT	2360	17595_S_AT
2263	13429_AT	2312	15465_AT	2361	17744_S_AT
2264	13472_AT	2313	15497_S_AT	2362	17758_AT
2265	13526_AT	2314	15589_S_AT	2363	17864_AT
2266	13569_AT	2315	15636_S_AT	2364	17868_AT
2267	13614_AT	2316	15663_S_AT	2365	17876_AT
2268	13686_S_AT	2317	15770_AT	2366	17894_AT
2269	13718_AT	2318	15792_AT	2367	17942_S_AT
2270	13719_AT	2319	15855_AT	2368	18008_R_AT
2271	13902_AT	2320	15860_AT	2369	18027_AT
2272	13918_AT	2321	15891_AT	2370	18053_S_AT
2273	13944_AT	2322	15898_AT	2371	18062_AT
2274	13964_AT	2323	15909_AT	2372	18082_AT

TABLE 7 (cont)

2373	18121_S_AT	2426	20648_S_AT
2374	18240_S_AT	2427	20668_AT
2375	18248_S_AT		
2376	18264_AT		
2377	18276_AT		
2378	18287_AT		
2379	18310_AT		
2380	18367_S_AT		
2381	18506_AT		
2382	18605_S_AT		
2383	18618_S_AT		
2384	18626_AT		
2385	18666_S_AT		
2386	18834_AT		
2387	18847_AT		
2388	18896_AT		
2389	18899_S_AT		
2390	18973_AT		
2391	18983_S_AT		
2392	18988_AT		
2393	18998_S_AT		
2394	19065_AT		
2395	19119_I_AT		
	19121_AT		
2396	19207_AT		
2397	19220_AT		
2398	19284_AT		
2399	19315_AT		
2400	19348_AT		
2401	19403_S_AT		
2402	19437_S_AT		
2403	19502_AT		
2404	19609_AT		
2405	19645_AT		
2406	19742_AT		
2407	19863_AT		
2408	19873_AT		
2409	19891_AT		
2410	20004_S_AT		
2411	20053_AT		
2412	20138_AT		
2413	20193_AT		
2414	20199_AT		
2415	20220_AT		
2416	20239_G_AT		
2417	20297_AT		
2418	20324_S_AT		
2419	20353_AT		
2420	20362_AT		
2421	20389_AT		
2422	20546_AT		
2423	20600_AT		
2424	20623_AT		
2425	20629_AT		

TABLE 8: 2X UP IN SALT, ONLY

12037_at	14570_at	16190_at	18506_at	20648_s_at
12137_at	14578_s_at	16196_at	18605_s_at	20678_at
12153_at	14596_at	16273_at	18626_at	20686_at
12186_at	14646_s_at	16314_at	18666_s_at	20707_s_at
12216_at	14662_f_at	16413_s_at	18747_f_at	
12268_at	14668_s_at	16414_at	18782_at	
12449_s_at	14729_s_at	16417_s_at	18834_at	
12470_at	14874_at	16455_at	18847_at	
12476_at	14888_at	16548_s_at	18913_s_at	
12487_at	14918_at	16582_s_at	18973_at	
12493_g_at	14952_at	16589_s_at	18988_at	
12609_at	14959_at	16594_s_at	18998_s_at	
12685_at	14986_at	16613_s_at	19065_at	
12704_f_at	15006_at	16651_s_at	19068_i_at	
12709_f_at	15042_at	16668_at	19123_at	
12734_f_at	15047_at	16690_g_at	19177_at	
12739_s_at	15062_at	16762_at	19220_at	
12750_s_at	15063_at	16820_at	19284_at	
12761_s_at	15108_s_at	16873_i_at	19288_at	
12819_at	15133_s_at	16987_s_at	19315_at	
12845_s_at	15147_s_at	16989_at	19437_s_at	
12946_at	15170_s_at	16995_at	19484_s_at	
13142_at	15175_s_at	17039_s_at	19502_at	
13198_i_at	15182_s_at	17040_s_at	19503_at	
13229_s_at	15190_s_at	17400_s_at	19592_at	
13275_f_at	15192_s_at	17425_s_at	19645_at	
13344_s_at	15324_at	17433_at	19742_at	
13370_at	15392_at	17467_at	19835_at	
13408_s_at	15424_at	17490_s_at	19873_at	
13464_at	15467_at	17529_s_at	19891_at	
13472_at	15497_s_at	17543_s_at	19992_at	
13526_at	15581_s_at	17566_at	20004_s_at	
13614_at	15623_f_at	17595_s_at	20053_at	
13652_at	15636_s_at	17744_s_at	20133_i_at	
13679_s_at	15646_s_at	17758_at	20138_at	
13751_at	15670_s_at	17855_at	20190_at	
13918_at	15770_at	17864_at	20199_at	
13919_at	15775_at	17876_at	20200_at	
13944_at	15778_at	18008_r_at	20297_at	
13964_at	15792_at	18013_r_at	20324_s_at	
13987_s_at	15855_at	18024_s_at	20335_s_at	
13993_s_at	15891_at	18027_at	20353_at	
14000_at	15909_at	18053_s_at	20362_at	
14032_at	15923_at	18078_at	20385_s_at	
14043_at	15969_s_at	18082_at	20389_at	
14052_at	15975_s_at	18090_s_at	20402_s_at	
14067_at	15995_s_at	18091_at	20450_at	
14070_at	15998_s_at	18121_s_at	20468_at	
14269_at	16017_at	18264_at	20489_at	
14285_at	16050_at	18276_at	20546_at	
14427_at	16067_s_at	18300_at	20569_s_at	
14501_at	16072_s_at	18367_s_at	20600_at	
14540_at	16165_s_at	18471_at	20623_at	

TABLE 9: 2X UP SALT, 3 HR ONLY

12037_at	15042_at	16987_s_at	20004_s_at
12137_at	15047_at	16989_at	20053_at
12153_at	15062_at	17039_s_at	20133_i_at
12186_at	15063_at	17040_s_at	20138_at
12216_at	15108_s_at	17425_s_at	20190_at
12268_at	15133_s_at	17433_at	20199_at
12470_at	15147_s_at	17490_s_at	20200_at
12476_at	15170_s_at	17543_s_at	20220_at
12487_at	15175_s_at	17744_s_at	20362_at
12493_g_at	15182_s_at	17864_at	20385_s_at
12609_at	15190_s_at	17876_at	20389_at
12685_at	15192_s_at	18008_r_at	20489_at
12704_f_at	15324_at	18013_r_at	20546_at
12709_f_at	15424_at	18024_s_at	20623_at
12734_f_at	15467_at	18027_at	20648_s_at
12739_s_at	15497_s_at	18053_s_at	20678_at
12750_s_at	15623_f_at	18078_at	20707_s_at
12819_at	15636_s_at	18082_at	
12946_at	15646_s_at	18090_s_at	
13142_at	15670_s_at	18091_at	
13229_s_at	15770_at	18121_s_at	
13275_f_at	15775_at	18264_at	
13370_at	15778_at	18276_at	
13408_s_at	15792_at	18367_s_at	
13464_at	15855_at	18471_at	
13472_at	15891_at	18506_at	
13614_at	15909_at	18605_s_at	
13652_at	15923_at	18626_at	
13679_s_at	15969_s_at	18666_s_at	
13918_at	15975_s_at	18747_f_at	
13919_at	15995_s_at	18782_at	
13944_at	15998_s_at	18834_at	
13987_s_at	16017_at	18847_at	
13993_s_at	16050_at	18913_s_at	
14000_at	16067_s_at	18973_at	
14032_at	16072_s_at	18988_at	
14043_at	16165_s_at	19065_at	
14052_at	16196_at	19068_i_at	
14067_at	16273_at	19123_at	
14269_at	16314_at	19177_at	
14285_at	16414_at	19220_at	
14501_at	16417_s_at	19288_at	
14540_at	16455_at	19315_at	
14570_at	16548_s_at	19437_s_at	
14596_at	16582_s_at	19484_s_at	
14668_s_at	16589_s_at	19502_at	
14729_s_at	16594_s_at	19503_at	
14888_at	16613_s_at	19592_at	
14918_at	16651_s_at	19645_at	
14952_at	16668_at	19742_at	
14959_at	16762_at	19835_at	
14986_at	16820_at	19873_at	
15006_at	16873_i_at	19891_at	

TABLE 10: 2X DOWN SALT, ONLY

12011_s_at	16046_s_at	20239_g_at
12180_at	16060_s_at	20433_at
12265_at	16088_f_at	20629_at
12335_at	16150_s_at	20668_at
12479_at	16166_s_at	
12562_at	16316_at	
12656_at	16340_at	
12813_at	16367_i_at	
13003_s_at	16426_at	
13052_s_at	16427_at	
13094_at	16436_at	
13178_at	16489_at	
13253_f_at	16502_at	
13387_at	16568_s_at	
13429_at	16638_s_at	
13472_at	16646_s_at	
13569_at	17273_at	
13686_s_at	17278_at	
13718_at	17567_at	
13719_at	17868_at	
13902_at	17880_s_at	
14003_at	17894_at	
14144_at	17901_at	
14267_at	17942_s_at	
14418_at	17960_at	
14544_at	17999_at	
14546_s_at	18062_at	
14636_s_at	18240_s_at	
14951_at	18248_s_at	
14956_s_at	18267_at	
14979_at	18279_s_at	
14990_at	18287_at	
15040_g_at	18310_at	
15049_at	18351_s_at	
15115_f_at	18455_at	
15137_s_at	18560_at	
15148_s_at	18571_at	
15176_s_at	18618_s_at	
15208_s_at	18896_at	
15371_at	18899_s_at	
15453_s_at	18967_s_at	
15463_at	18983_s_at	
15465_at	19119_i_at	
15589_s_at	19121_at	
15663_s_at	19207_at	
15860_at	19348_at	
15898_at	19403_s_at	
15931_at	19609_at	
15965_at	19742_at	
15970_s_at	19826_at	
15972_s_at	19863_at	
16005_s_at	19883_at	
16028_at	20193_at	

TABLE 11

OSMOTIC STRESS RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:
2428	11994_AT
2429	12028_AT
2430	12033_AT
2431	12039_AT
2432	12068_AT
2433	12096_AT
2434	12110_AT
2435	12114_AT
2436	12135_AT
2437	12139_AT
2438	12189_AT
2439	12191_AT
2440	12211_AT
2441	12223_S_AT
2442	12366_S_AT
	12869_S_AT
2443	12381_AT
2444	12406_S_AT
2445	12412_AT
2446	12453_AT
2447	12571_S_AT
2448	12662_AT
2449	12746_I_AT
2450	12774_AT
2451	12787_AT
2452	12847_AT
2453	12848_AT
2454	12895_AT
2455	12911_S_AT
2456	12920_AT
	12921_S_AT
2457	13027_AT
2458	13059_AT
2459	13075_I_AT
2460	13180_S_AT
2461	13255_I_AT
2462	13270_AT
	18167_S_AT
2463	13283_S_AT
2464	13382_AT
2465	13386_S_AT
2466	13433_AT
2467	13482_AT
2468	13732_AT
2469	13733_I_AT
2470	13842_AT
2471	13860_S_AT
2472	13868_AT
2473	13901_AT
2474	13933_AT
2475	13995_AT
2476	14062_AT
2477	14118_I_AT
2478	14141_AT
2479	14310_AT
2480	14354_AT
2481	14476_AT
2482	14513_S_AT
2483	14568_S_AT
2484	14604_AT
2485	14634_S_AT
2486	14660_S_AT
2487	14666_S_AT
2488	14686_S_AT
	17464_AT
2489	14726_S_AT
2490	14848_S_AT
2491	14873_AT
2492	14883_AT
2493	15082_AT
2494	15121_S_AT
	16014_S_AT
2495	15168_S_AT
2496	15271_AT
2497	15338_AT
2498	15418_AT
2499	15429_AT
2500	15548_AT
2501	15666_S_AT
2502	15672_S_AT
2503	15680_S_AT
2504	15867_AT
2505	15918_AT
2506	15999_S_AT
2507	16303_AT
2508	16363_AT
2509	16440_S_AT
2510	16458_S_AT
2511	16475_AT
2512	16513_S_AT
2513	16529_AT
2514	16547_S_AT
2515	16553_F_AT
2516	16563_S_AT
2517	16629_S_AT
2518	16797_AT
2519	16814_AT
2520	16832_AT
2521	16976_S_AT
2522	17007_AT
2523	17037_S_AT
2524	17054_S_AT
2525	17257_S_AT
	18725_S_AT
2526	17270_AT
2527	17275_I_AT
2528	17376_AT
2529	17378_AT
2530	17468_AT
2531	17481_AT
2532	17511_S_AT
2533	17519_S_AT
2534	17815_S_AT
2535	17897_AT
2536	17923_S_AT
2537	17934_AT
2538	17937_S_AT
2539	17944_AT
2540	17958_AT
2541	18216_AT
2542	18227_AT
2543	18284_AT
2544	18301_S_AT
2545	18312_S_AT
2546	18326_S_AT
2547	18369_AT
2548	18411_AT
2549	18533_AT
2550	18576_S_AT
2551	18599_AT
2552	18640_AT
2553	18672_S_AT
2554	18720_S_AT
2555	18768_AT
2556	18877_AT
2557	18942_AT
2558	18945_AT
2559	18960_AT
2560	18965_AT
2561	19060_AT
2562	19164_G_AT
2563	19266_AT
2564	19366_S_AT
2565	19369_AT
2566	19371_AT
2567	19386_AT
2568	19412_AT
2569	19427_S_AT
2570	19622_G_AT
2571	19681_AT

TABLE 11 (cont)

2572	19819_S_AT
2573	19961_S_AT
2574	20002_AT
2575	20034_I_AT
2576	20062_AT
2577	20136_AT
2578	20223_AT
2579	20235_I_AT
2580	20401_AT
2581	20407_AT
2582	20470_AT
2583	20626_AT
2584	20631_S_AT
2585	20647_AT

TABLE 12: 2X UP IN MANNITOL, ONLY

12039_at	16832_at
12068_at	16993_at
12139_at	17037_s_at
12212_at	17054_s_at
12278_at	17083_s_at
12366_s_at	17097_s_at
12453_at	17119_s_at
12556_at	17270_at
12575_s_at	17305_at
12746_i_at	17376_at
12848_at	17378_at
12869_s_at	17449_s_at
12920_at	17481_at
12921_s_at	17533_s_at
13041_s_at	17832_s_at
13059_at	17923_s_at
13241_s_at	17944_at
13255_i_at	18059_i_at
13270_at	18216_at
13382_at	18230_at
13406_at	18255_at
13433_at	18284_at
13550_at	18301_s_at
13672_s_at	18312_s_at
13716_at	18326_s_at
13842_at	18599_at
13933_at	18672_s_at
13995_at	18720_s_at
14062_at	18768_at
14075_at	18814_at
14162_at	18877_at
14208_at	18921_g_at
14217_at	18960_at
14235_at	19060_at
14310_at	19182_at
14431_at	19192_at
14513_s_at	19266_at
14584_at	19369_at
14604_at	19386_at
14673_s_at	19402_at
14856_s_at	19412_at
15207_s_at	19432_s_at
15338_at	19469_at
15406_at	19622_g_at
15418_at	19819_s_at
15591_s_at	19826_at
15666_s_at	20152_at
15680_s_at	20223_at
15866_s_at	20235_i_at
15918_at	20365_s_at
16340_at	20470_at
16553_f_at	20537_at
16797_at	20547_at

TABLE 13: 2X UP IN MANNITOL, 3 HR ONLY

12039_at	17449_s_at
12068_at	17481_at
12139_at	17533_s_at
12212_at	17923_s_at
12278_at	17944_at
12366_s_at	18059_i_at
12453_at	18216_at
12556_at	18230_at
12575_s_at	18255_at
12746_i_at	18301_s_at
12848_at	18312_s_at
12869_s_at	18326_s_at
12920_at	18599_at
12921_s_at	18720_s_at
13041_s_at	18768_at
13059_at	18814_at
13241_s_at	18877_at
13382_at	18921_g_at
13406_at	18960_at
13433_at	19060_at
13550_at	19192_at
13672_s_at	19266_at
13933_at	19369_at
13995_at	19386_at
14062_at	19402_at
14075_at	19412_at
14162_at	19432_s_at
14217_at	19469_at
14310_at	19622_g_at
14431_at	19819_s_at
14513_s_at	20152_at
14584_at	20223_at
14604_at	20235_i_at
14673_s_at	20365_s_at
14856_s_at	20470_at
15207_s_at	20537_at
15338_at	
15418_at	
15591_s_at	
15866_s_at	
15918_at	
16340_at	
16553_f_at	
16797_at	
16832_at	
17037_s_at	
17054_s_at	
17083_s_at	
17097_s_at	
17270_at	
17305_at	
17376_at	
17378_at	

TABLE 14: 2X DOWN IN MANNITOL, ONLY

12028_at	14897_at	17958_at
12033_at	14918_at	18012_s_at
12110_at	15082_at	18227_at
12114_at	15084_at	18272_at
12189_at	15098_s_at	18331_s_at
12191_at	15105_s_at	18369_at
12211_at	15121_s_at	18411_at
12223_s_at	15126_s_at	18533_at
12268_at	15168_s_at	18576_s_at
12345_at	15271_at	18640_at
12381_at	15429_at	18696_s_at
12406_s_at	15548_at	18945_at
12412_at	15672_s_at	18949_at
12522_at	15753_at	18953_at
12571_s_at	15867_at	18965_at
12662_at	15999_s_at	19164_g_at
12787_at	16001_at	19322_at
12847_at	16021_s_at	19366_s_at
12895_at	16190_at	19371_at
12911_s_at	16260_at	19397_at
13027_at	16303_at	19427_s_at
13075_i_at	16363_at	19681_at
13221_at	16458_s_at	19707_s_at
13262_s_at	16468_at	19839_at
13283_s_at	16475_at	19961_s_at
13386_s_at	16513_s_at	19976_at
13447_s_at	16529_at	19998_at
13482_at	16563_s_at	20002_at
13634_s_at	16690_g_at	20034_i_at
13709_s_at	16814_at	20136_at
13732_at	16847_at	20382_s_at
13733_i_at	16927_s_at	20407_at
13812_s_at	16976_s_at	20529_at
13825_s_at	17007_at	20626_at
13860_s_at	17014_s_at	20631_s_at
13868_at	17016_s_at	20647_at
13901_at	17071_s_at	20699_at
14052_at	17090_s_at	
14224_at	17257_s_at	
14244_s_at	17275_i_at	
14254_s_at	17424_at	
14256_f_at	17464_at	
14354_at	17468_at	
14476_at	17511_s_at	
14568_s_at	17519_s_at	
14634_s_at	17525_s_at	
14646_s_at	17645_s_at	
14660_s_at	17741_at	
14686_s_at	17815_s_at	
14726_s_at	17897_at	
14848_s_at	17899_at	
14873_at	17934_at	
14883_at	17937_s_at	

TABLE 15

COLD & OSOMOTIC STRESS RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:
1699	12040_AT
1700	12048_AT
1701	12054_S_AT
1702	12077_AT
1703	12107_I_AT
1704	12113_AT
1705	12154_AT
1706	12171_AT
1707	12212_AT
1708	12278_AT
1709	12317_AT
1710	12325_AT
1711	12333_AT
1712	12345_AT
1713	12349_S_AT
	14254_S_AT
	14256_F_AT
1714	12356_AT
1715	12380_AT
1716	12392_AT
1717	12460_S_AT
1718	12556_AT
1719	12575_S_AT
1720	12686_S_AT
1721	12701_I_AT
1722	12754_G_AT
1723	12782_R_AT
1724	12784_AT
1725	12879_S_AT
1726	12891_AT
	16817_S_AT
1727	12898_G_AT
1728	12974_AT
1729	12998_AT
1730	13041_S_AT
1731	13124_AT
1732	13134_S_AT
1733	13144_AT
1734	13147_AT
1735	13152_S_AT
1736	13187_I_AT
	16981_S_AT
1737	13192_S_AT
	17525_S_AT
1738	13212_S_AT
1739	13215_S_AT
	16649_S_AT
1740	13241_S_AT
1741	13246_AT
1742	13262_S_AT
1743	13286_S_AT
1744	13324_AT
1745	13340_S_AT
1746	13361_AT
1747	13406_AT
1748	13441_S_AT
1749	13513_AT
1750	13550_AT
1751	13573_AT
1752	13577_S_AT
1753	13606_AT
1754	13609_AT
1755	13625_S_AT
1756	13626_AT
1757	13634_S_AT
1758	13672_S_AT
	18916_S_AT
1759	13709_S_AT
1760	13736_AT
1761	13775_AT
1762	13810_AT
1763	13812_S_AT
1764	13825_S_AT
1765	14015_S_AT
	14016_S_AT
1766	14029_AT
1767	14036_AT
1768	14051_AT
1769	14060_AT
1770	14064_AT
1771	14066_AT
1772	14075_AT
1773	14094_S_AT
	19999_S_AT
1774	14096_AT
1775	14104_AT
1776	14123_S_AT
1777	14126_S_AT
1778	14131_AT
1779	14136_AT
1780	14139_AT
	14140_AT
1781	14162_AT
	14217_AT
1782	14178_AT
1783	14201_AT
1784	14208_AT
1785	14235_AT
1786	14242_S_AT
1787	14431_AT
1788	14480_AT
1789	14497_AT
1790	14553_AT
1791	14584_AT
1792	14600_AT
1793	14673_S_AT
	19432_S_AT
1794	14681_G_AT
1795	14699_AT
1796	14751_AT
1797	14762_AT
1798	14828_S_AT
1799	14856_S_AT
1800	14882_AT
1801	14897_AT
1802	14978_AT
1803	14985_S_AT
1804	15031_AT
1805	15084_AT
1806	15096_AT
1807	15105_S_AT
1808	15110_S_AT
1809	15111_S_AT
1810	15120_S_AT
1811	15126_S_AT
1812	15142_S_AT
1813	15144_S_AT
1814	15184_S_AT
1815	15198_S_AT
1816	15203_S_AT
1817	15207_S_AT
1818	15240_AT
1819	15366_AT
1820	15398_AT
1821	15406_AT
1822	15448_AT
1823	15466_AT
1824	15481_AT
1825	15484_AT
1826	15549_AT
1827	15591_S_AT
1828	15606_S_AT
1829	15614_S_AT
	16927_S_AT
1830	15629_S_AT
1831	15633_S_AT
1832	15641_S_AT
	18012_S_AT
1833	15720_AT

TABLE 15 (cont)

1834	15815_S_AT
1835	15817_AT
1836	15837_AT
1837	15841_AT
1838	15866_S_AT
	18255_AT
1839	15872_AT
	18331_S_AT
1840	15892_AT
1841	15933_AT
1842	15947_AT
1843	15959_S_AT
1844	16001_AT
1845	16052_AT
1846	16161_S_AT
1847	16204_AT
1848	16232_S_AT
1849	16252_AT
1850	16260_AT
1851	16266_AT
1852	16299_AT
1853	16365_AT
1854	16468_AT
1855	16477_AT
1856	16491_AT
1857	16523_S_AT
1858	16566_S_AT
1859	16570_S_AT
1860	16688_AT
1861	16840_AT
1862	16847_AT
1863	16893_AT
1864	16896_S_AT
1865	16898_S_AT
1866	16912_S_AT
1867	16980_AT
1868	16993_AT
1869	17008_AT
1870	17012_S_AT
1871	17014_S_AT
1872	17016_S_AT
1873	17032_S_AT
1874	17050_S_AT
	17051_S_AT
1875	17071_S_AT
1876	17090_S_AT
	18690_S_AT
1877	17097_S_AT
1878	17104_S_AT
1879	17119_S_AT
1880	17160_AT
1881	17305_AT
1882	17424_AT
1883	17449_S_AT
1884	17452_G_AT
1885	17540_S_AT
1886	17552_S_AT
1887	17571_AT
1888	17589_AT
1889	17641_G_AT
1890	17741_AT
	18098_AT
1891	17766_AT
1892	17873_S_AT
1893	17904_AT
1894	17920_S_AT
1895	17925_AT
1896	17943_AT
1897	18059_I_AT
1898	18230_AT
1899	18263_AT
1900	18272_AT
1901	18540_AT
1902	18608_AT
1903	18647_AT
1904	18662_S_AT
1905	18664_AT
1906	18695_S_AT
1907	18704_AT
1908	18814_AT
1909	18907_S_AT
1910	18921_G_AT
1911	18924_AT
1912	18949_AT
	19707_S_AT
1913	18995_AT
1914	19017_AT
1915	19034_AT
1916	19063_AT
1917	19142_AT
1918	19158_AT
1919	19180_AT
1920	19187_AT
1921	19192_AT
1922	19195_AT
1923	19199_AT
1924	19231_AT
1925	19263_AT
1926	19308_AT
1927	19322_AT
1928	19365_S_AT
1929	19372_AT
1930	19389_AT
1931	19392_AT
1932	19397_AT
1933	19400_AT
1934	19402_AT
1935	19458_AT
1936	19469_AT
1937	19473_AT
1938	19597_S_AT
1939	19710_S_AT
1940	19830_AT
1941	19839_AT
1942	19840_S_AT
1943	19853_AT
1944	19860_AT
1945	19880_AT
1946	19889_AT
1947	19898_AT
1948	19914_AT
1949	19924_AT
1950	19949_AT
1951	19976_AT
1952	19998_AT
1953	20030_AT
1954	20151_AT
1955	20152_AT
1956	20187_AT
1957	20214_I_AT
1958	20269_AT
1959	20271_AT
1960	20273_AT
1961	20299_AT
1962	20323_AT
1963	20429_S_AT
1964	20457_AT
1965	20480_S_AT
1966	20529_AT
1967	20547_AT
1968	20555_S_AT
1969	20699_AT

TABLE 16: 2X UP IN MANNITOL & COLD, ONLY

12345_at	17066_s_at
12784_at	17540_s_at
13153_r_at	17567_at
13212_s_at	17766_at
13215_s_at	17904_at
13246_at	17920_s_at
13262_s_at	17943_at
13361_at	18263_at
13625_s_at	18351_s_at
13764_at	18662_s_at
13810_at	18670_g_at
14015_s_at	18695_s_at
14016_s_at	18704_at
14060_at	18729_at
14096_at	18995_at
14123_s_at	19158_at
14139_at	19473_at
14219_at	19710_s_at
14248_at	19883_at
14254_s_at	19889_at
14256_f_at	20030_at
14609_at	20269_at
14636_s_at	20271_at
14681_g_at	20299_at
14699_at	20429_s_at
14704_s_at	20438_at
14828_s_at	20480_s_at
14882_at	
15110_s_at	
15184_s_at	
15448_at	
15629_s_at	
15720_at	
15846_at	
15947_at	
16161_s_at	
16365_at	
16427_at	
16566_s_at	
16570_s_at	
16649_s_at	
16688_at	
16712_at	
16817_s_at	
16840_at	
16893_at	
16912_s_at	
16916_s_at	
16927_s_at	
16981_s_at	
17012_s_at	
17014_s_at	
17051_s_at	

TABLE 17: 2X DOWN COLD & MANNITOL, ONLY

12040_at	14553_at	17873_s_at
12048_at	14612_at	17925_at
12054_s_at	14751_at	18098_at
12077_at	14762_at	18540_at
12107_i_at	14978_at	18608_at
12113_at	14985_s_at	18647_at
12154_at	15031_at	18664_at
12171_at	15096_at	18690_s_at
12317_at	15111_s_at	18725_s_at
12325_at	15120_s_at	18924_at
12333_at	15142_s_at	19017_at
12356_at	15198_s_at	19034_at
12380_at	15203_s_at	19063_at
12392_at	15240_at	19141_at
12460_s_at	15366_at	19142_at
12686_s_at	15392_at	19180_at
12701_i_at	15398_at	19187_at
12782_r_at	15466_at	19195_at
12879_s_at	15481_at	19199_at
12898_g_at	15484_at	19231_at
12974_at	15549_at	19308_at
12998_at	15623_f_at	19372_at
13144_at	15815_s_at	19392_at
13147_at	15817_at	19400_at
13152_s_at	15841_at	19458_at
13192_s_at	15892_at	19597_s_at
13286_s_at	15933_at	19762_at
13324_at	15959_s_at	19830_at
13340_s_at	16052_at	19853_at
13441_s_at	16204_at	19869_at
13513_at	16252_at	19880_at
13573_at	16266_at	19898_at
13606_at	16299_at	19914_at
13609_at	16477_at	19924_at
13626_at	16491_at	19949_at
13736_at	16561_s_at	20151_at
13775_at	16645_s_at	20187_at
14029_at	16898_s_at	20214_i_at
14036_at	16980_at	20273_at
14051_at	17008_at	20323_at
14064_at	17104_s_at	20457_at
14066_at	17160_at	20555_s_at
14094_s_at	17317_at	
14104_at	17400_s_at	
14126_s_at	17452_g_at	
14131_at	17477_s_at	
14136_at	17500_s_at	
14178_at	17552_s_at	
14192_at	17571_at	
14201_at	17572_s_at	
14242_s_at	17589_at	
14480_at	17641_g_at	
14497_at	17855_at	

TABLE 18

COLD & SALINE STRESS RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:
1970	12021_AT
1971	12037_AT
1972	12094_AT
1973	12098_AT
1974	12128_AT
1975	12148_AT
1976	12151_AT
1977	12357_S_AT
1978	12394_AT
1979	12472_S_AT
1980	12475_AT
1981	12482_S_AT
1982	12490_AT
1983	12505_S_AT
1984	12531_AT
1985	12540_S_AT
1986	12541_AT
1987	12577_AT
1988	12594_AT
1989	12629_AT
1990	12642_AT
1991	12656_AT
1992	12660_AT
1993	12712_F_AT
1994	12725_R_AT
1995	12745_AT
1996	12777_I_AT
1997	12790_S_AT
1998	12798_AT
1999	12801_AT
2000	12855_F_AT
2001	12887_S_AT
2002	12933_R_AT
2003	12951_AT
2004	13005_AT
2005	13015_S_AT
2006	13115_AT
2007	13178_AT
2008	13228_AT
2009	13236_S_AT
	16646_S_AT
2010	13266_S_AT
	15211_S_AT
2011	13275_F_AT
2012	13335_AT
2013	13362_S_AT
2014	13428_AT
2015	13464_AT
2016	13480_AT
2017	13538_AT
2018	13544_AT
2019	13549_AT
2020	13565_AT
SEQ ID NO:	AFFYMETRIX ID NO:
2021	13580_AT
2022	13588_AT
2023	13649_AT
2024	13652_AT
2025	13679_S_AT
2026	13696_AT
2027	13702_S_AT
2028	13751_AT
2029	13919_AT
2030	13943_AT
2031	13950_S_AT
2032	14050_AT
2033	14055_S_AT
	16166_S_AT
2034	14067_AT
2035	14078_AT
2036	14110_I_AT
2037	14144_AT
2038	14232_AT
2039	14285_AT
2040	14346_AT
2041	14432_AT
2042	14468_AT
2043	14479_AT
2044	14524_S_AT
2045	14608_AT
2046	14621_AT
2047	14635_S_AT
	17128_S_AT
2048	14640_S_AT
2049	14643_S_AT
2050	14663_S_AT
2051	14668_S_AT
2052	14688_S_AT
	18279_S_AT
2053	14737_S_AT
2054	14768_AT
2055	14875_AT
2056	14911_S_AT
	17056_S_AT
2057	14924_AT
2058	14956_S_AT
	15148_S_AT
	18673_AT
2059	14964_AT
2060	15022_AT
2061	15040_G_AT
2062	15047_AT
2063	15063_AT
2064	15085_S_AT
2065	15123_S_AT
2066	15133_S_AT
2067	15137_S_AT
SEQ ID NO:	AFFYMETRIX ID NO:
2068	15153_S_AT
2069	15170_S_AT
2070	15172_S_AT
2071	15182_S_AT
2072	15190_S_AT
2073	15241_S_AT
2074	15389_AT
2075	15453_S_AT
2076	15495_AT
2077	15496_AT
2078	15519_S_AT
2079	15562_AT
2080	15580_S_AT
2081	15582_S_AT
2082	15638_S_AT
	18751_F_AT
2083	15646_S_AT
2084	15647_S_AT
2085	15654_S_AT
2086	15655_S_AT
2087	15658_S_AT
2088	15670_S_AT
2089	15775_AT
2090	15798_AT
2091	15930_AT
2092	15931_AT
2093	15949_S_AT
2094	16017_AT
2095	16053_I_AT
2096	16078_S_AT
2097	16086_S_AT
2098	16120_S_AT
2099	16126_S_AT
2100	16150_S_AT
2101	16159_S_AT
2102	16230_AT
2103	16306_AT
2104	16367_I_AT
2105	16417_S_AT
	18083_R_AT
2106	16418_S_AT
2107	16423_AT
2108	16449_S_AT
2109	16484_S_AT

TABLE 18 (cont)

2110	16489_AT	2163	18455_AT	2218	20565_AT
2111	16565_S_AT	2164	18459_AT	2219	20570_AT
2112	16596_S_AT	2165	18571_AT	2220	20576_AT
2113	16600_S_AT	2166	18604_AT	2221	20577_AT
2114	16603_S_AT		19181_S_AT	2222	20609_AT
2115	16638_S_AT	2167	18644_AT	2223	20646_AT
2116	16642_S_AT	2168	18745_F_AT	2224	20672_AT
2117	16763_AT		19611_S_AT	2225	20707_S_AT
2118	16914_S_AT	2169	18782_AT	2226	20720_AT
2119	16968_AT	2170	18881_AT		
2120	16983_AT	2171	18904_S_AT		
2121	16989_AT	2172	18914_S_AT		
2122	17002_AT	2173	18963_AT		
2123	17015_S_AT	2174	19068_I_AT		
2124	17040_S_AT	2175	19078_AT		
	18913_S_AT	2176	19171_AT		
2125	17232_AT	2177	19177_AT		
2126	17380_AT	2178	19394_AT		
2127	17394_S_AT	2179	19411_AT		
	20640_S_AT	2180	19415_AT		
2128	17398_AT	2181	19466_S_AT		
2129	17448_AT	2182	19484_S_AT		
2130	17485_S_AT	2183	19549_S_AT		
2131	17490_S_AT	2184	19592_AT		
2132	17499_S_AT	2185	19633_AT		
2133	17505_S_AT	2186	19641_AT		
2134	17516_S_AT	2187	19669_AT		
2135	17529_S_AT	2188	19672_AT		
2136	17543_S_AT	2189	19684_AT		
2137	17593_R_AT	2190	19692_AT		
	19858_S_AT	2191	19746_AT		
2138	17609_AT	2192	19835_AT		
2139	17698_AT	2193	19848_S_AT		
2140	17836_AT	2194	19892_AT		
2141	17886_AT	2195	19904_AT		
2142	17896_AT	2196	19936_AT		
2143	17901_AT	2197	19974_S_AT		
2144	17902_S_AT	2198	19994_AT		
2145	17913_S_AT	2199	20005_S_AT		
2146	17924_AT	2200	20022_AT		
2147	17954_S_AT	2201	20032_AT		
2148	17960_AT	2202	20044_AT		
2149	17991_G_AT	2203	20049_AT		
	18967_S_AT	2204	20081_AT		
2150	17999_AT	2205	20133_I_AT		
2151	18057_I_AT	2206	20155_S_AT		
2152	18078_AT	2207	20163_S_AT		
2153	18091_AT	2208	20200_AT		
2154	18168_S_AT	2209	20296_S_AT		
2155	18252_AT	2210	20336_AT		
2156	18267_AT	2211	20341_AT		
2157	18300_AT	2212	20372_AT		
2158	18308_I_AT	2213	20385_S_AT		
2159	18328_AT	2214	20433_AT		
2160	18354_AT	2215	20489_AT		
2161	18402_AT	2216	20525_AT		
2162	18416_AT	2217	20543_AT		

TABLE 19: 2X UP IN SALT & COLD, ONLY

12004_at	15495_at	18745_f_at
12098_at	15496_at	18904_s_at
12148_at	15519_s_at	18914_s_at
12251_at	15580_s_at	18929_s_at
12357_s_at	15582_s_at	18946_at
12394_at	15776_at	18963_at
12457_at	15798_at	19078_at
12505_s_at	15910_at	19137_at
12522_at	15931_at	19141_at
12541_at	15937_at	19411_at
12594_at	15949_s_at	19641_at
12606_at	15972_s_at	19672_at
12697_at	16048_at	19684_at
12745_at	16086_s_at	19692_at
12781_at	16120_s_at	19746_at
12798_at	16126_s_at	19762_at
12855_f_at	16150_s_at	19869_at
12945_at	16159_s_at	19894_at
12951_at	16230_at	19904_at
13005_at	16306_at	19936_at
13015_s_at	16418_s_at	19994_at
13115_at	16423_at	20005_s_at
13146_s_at	16449_s_at	20031_at
13335_at	16565_s_at	20044_at
13447_s_at	16603_s_at	20382_s_at
13480_at	16763_at	20406_g_at
13544_at	16968_at	20421_at
13549_at	16983_at	20525_at
13580_at	17002_at	20543_at
13649_at	17015_s_at	20565_at
13943_at	17019_s_at	20570_at
13950_s_at	17078_s_at	20640_s_at
14110_i_at	17232_at	20646_at
14144_at	17317_at	20720_at
14224_at	17394_s_at	
14432_at	17516_s_at	
14468_at	17585_s_at	
14479_at	17609_at	
14524_s_at	17698_at	
14640_s_at	17836_at	
14643_s_at	17896_at	
14735_s_at	17899_at	
14737_s_at	17902_s_at	
14768_at	17960_at	
14784_at	17963_at	
14924_at	18168_s_at	
15064_at	18252_at	
15127_s_at	18267_at	
15186_s_at	18308_i_at	
15189_s_at	18354_at	
15255_at	18402_at	
15389_at	18459_at	
15482_at	18484_at	

TABLE 20: 2X DOWN IN COLD & SALT, ONLY

12021_at	15123_s_at	19394_at
12094_at	15153_s_at	19415_at
12128_at	15172_s_at	19466_s_at
12151_at	15190_s_at	19549_s_at
12332_s_at	15211_s_at	19592_at
12472_s_at	15241_s_at	19633_at
12475_at	15437_at	19669_at
12482_s_at	15562_at	19848_s_at
12490_at	15638_s_at	19858_s_at
12531_at	15647_s_at	19878_at
12540_s_at	15654_s_at	19892_at
12577_at	15655_s_at	19974_s_at
12629_at	15658_s_at	20022_at
12642_at	15695_s_at	20032_at
12660_at	15846_at	20049_at
12676_s_at	15930_at	20081_at
12712_f_at	16053_i_at	20155_s_at
12725_r_at	16078_s_at	20163_s_at
12777_i_at	16229_at	20296_s_at
12790_s_at	16465_at	20336_at
12801_at	16484_s_at	20341_at
12887_s_at	16596_s_at	20365_s_at
12933_r_at	16600_s_at	20372_at
13153_r_at	16642_s_at	20489_at
13228_at	16914_s_at	20491_at
13362_s_at	17027_s_at	20576_at
13428_at	17066_s_at	20577_at
13538_at	17083_s_at	20609_at
13565_at	17128_s_at	20672_at
13588_at	17380_at	
13696_at	17398_at	
13702_s_at	17448_at	
13716_at	17485_s_at	
13764_at	17490_s_at	
14050_at	17499_s_at	
14055_s_at	17505_s_at	
14069_at	17514_s_at	
14078_at	17593_r_at	
14232_at	17886_at	
14346_at	17913_s_at	
14608_at	17924_at	
14609_at	17954_s_at	
14621_at	17991_g_at	
14635_s_at	18057_i_at	
14663_s_at	18069_at	
14688_s_at	18328_at	
14691_at	18416_at	
14704_s_at	18604_at	
14875_at	18644_at	
14911_s_at	18881_at	
14964_at	19171_at	
15022_at	19181_s_at	
15085_s_at	19182_at	

TABLE 21

OSMOTIC & SALINE STRESS RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:
2586	12126_S_AT
2587	12137_AT
2588	12227_AT
2589	12239_AT
2590	12268_AT
2591	12369_AT
2592	12476_AT
2593	12484_G_AT
2594	12494_AT
2595	12644_AT
2596	12645_AT
2597	12796_S_AT
2598	12819_AT
2599	12841_AT
2600	12852_S_AT
	19455_S_AT
2601	13084_AT
2602	13171_AT
2603	13174_R_AT
2604	13596_AT
2605	13807_AT
2606	13977_AT
2607	13999_AT
2608	14052_AT
2609	14293_AT
2610	14335_AT
2611	14486_AT
2612	14506_AT
2613	14518_AT
2614	14540_AT
2615	14578_S_AT
2616	14646_S_AT
2617	14662_F_AT
	15962_S_AT
2618	14901_AT
2619	14918_AT
2620	14986_AT
2621	15053_S_AT
2622	15179_S_AT
2623	15252_G_AT
2624	15280_AT
2625	15467_AT
2626	15607_S_AT
2627	15625_S_AT
2628	15703_I_AT
2629	15827_AT
2630	15863_AT
2631	15923_AT
2632	15946_S_AT
2633	16005_S_AT
2634	16073_F_AT
2635	16114_S_AT
2636	16127_S_AT
	18744_F_AT
2637	16190_AT
2638	16196_AT
2639	16236_G_AT
	19531_AT
2640	16310_AT
2641	16316_AT
2642	16334_S_AT
2643	16335_AT
2644	16340_AT
2645	16450_S_AT
2646	16500_AT
2647	16524_AT
2648	16533_AT
2649	16690_G_AT
2650	16762_AT
2651	16819_AT
2652	16873_I_AT
2653	16972_AT
2654	16991_AT
2655	17099_S_AT
2656	17339_AT
2657	17397_S_AT
2658	17419_AT
2659	17460_AT
2660	17554_S_AT
2661	17939_AT
2662	18013_R_AT
	18178_S_AT
2663	18024_S_AT
2664	18032_I_AT
2665	18054_AT
2666	18151_AT
2667	18281_AT
2668	18445_AT
2669	18520_AT
2670	18583_AT
2671	18663_S_AT
2672	18753_S_AT
2673	18876_AT
2674	18938_G_AT
2675	18971_AT
2676	18977_AT
2677	18981_AT
2678	19099_AT
2679	19196_AT
2680	19376_AT
2681	19409_AT
2682	19503_AT
2683	19826_AT
2684	19847_S_AT
2685	19930_AT
2686	19992_AT
2687	20096_AT
2688	20108_AT
2689	20256_S_AT
2690	20290_S_AT
2691	20298_AT
2692	20305_AT
2693	20322_AT
2694	20333_AT
2695	20402_S_AT
2696	20424_AT
2697	20446_S_AT
2698	20450_AT
2699	20468_AT
2700	20569_S_AT
2701	20639_AT
2702	20678_AT
2703	20686_AT

TABLE 22: 2X UP IN SALT & MANNITOL, ONLY

12126_s_at	17548_s_at
12227_at	17554_s_at
12369_at	17961_at
12521_at	18032_i_at
12644_at	18054_at
12645_at	18151_at
12724_f_at	18167_s_at
12795_at	18281_at
12796_s_at	18520_at
12841_at	18663_s_at
12852_s_at	18744_f_at
12958_at	18753_s_at
13014_at	18789_at
13174_r_at	18876_at
13211_s_at	18909_s_at
13596_at	18938_g_at
13640_at	18977_at
13789_at	19099_at
13977_at	19108_at
13999_at	19135_at
14069_at	19227_at
14083_at	19376_at
14089_at	19429_at
14293_at	19455_s_at
14675_s_at	19531_at
15053_s_at	19789_s_at
15058_s_at	19878_at
15252_g_at	20017_at
15280_at	20096_at
15437_at	20256_s_at
15607_s_at	20290_s_at
15625_s_at	20305_at
15827_at	20322_at
15863_at	20333_at
15880_at	20420_at
16005_s_at	20424_at
16031_at	20689_s_at
16073_f_at	
16316_at	
16334_s_at	
16335_at	
16450_s_at	
16500_at	
16524_at	
16533_at	
16597_s_at	
16819_at	
17085_s_at	
17099_s_at	
17339_at	
17419_at	
17442_i_at	
17514_s_at	

TABLE 23: 2X DOWN IN MANNITOL & SALT, ONLY

12239_at
12251_at
12476_at
12484_g_at
12494_at
12561_at
12647_s_at
12719_f_at
12819_at
12841_at
13084_at
13171_at
13172_s_at
13435_at
13807_at
14250_r_at
14335_at
14486_at
14506_at
14518_at
14901_at
15046_s_at
15179_s_at
15451_at
15703_i_at
15946_s_at
16014_s_at
16114_s_at
16310_at
16342_at
16712_at
16762_at
16972_at
16991_at
17397_s_at
17408_at
17460_at
17775_at
17939_at
18445_at
18583_at
18751_f_at
18971_at
18981_at
19156_s_at
19196_at
19359_s_at
19409_at
19503_at
19713_at
19718_at
19847_s_at
19930_at
20108_at
20298_at
20421_at
20432_at
20446_s_at
20639_at

TABLE 24

COLD, OSMOTIC & SALINE RESPONSIVE SEQUENCES

SEQ ID NO:	AFFYMETRIX ID NO:
1262	12004_AT
1263	12023_S_AT
1264	12078_AT
1265	12115_AT
1266	12118_AT
1267	12150_AT
1268	12251_AT
1269	12271_S_AT
1270	12276_AT
1271	12332_S_AT
	13211_S_AT
1272	12338_AT
1273	12400_AT
1274	12430_AT
1275	12457_AT
1276	12521_AT
1277	12522_AT
1278	12530_AT
1279	12536_S_AT
1280	12538_AT
1281	12561_AT
1282	12574_AT
	19019_I_AT
1283	12595_AT
1284	12606_AT
1285	12609_AT
1286	12622_AT
1287	12630_AT
1288	12647_S_AT
1289	12676_S_AT
1290	12697_AT
1291	12698_AT
1292	12719_F_AT
1293	12724_F_AT
	15871_S_AT
	16597_S_AT
1294	12749_AT
1295	12765_AT
1296	12769_AT
1297	12781_AT
1298	12785_AT
1299	12792_S_AT
1300	12795_AT
1301	12805_S_AT
1302	12857_AT
1303	12883_S_AT
1304	12909_S_AT
	16539_S_AT
1305	12932_S_AT
	15605_S_AT
1306	12945_AT
1307	12958_AT
1308	12964_AT
1309	12968_AT
1310	12972_AT
1311	12989_S_AT
1312	13004_AT
1313	13014_AT
1314	13025_AT
1315	13036_AT
1316	13099_S_AT
1317	13136_AT
1318	13146_S_AT
	13239_S_AT
1319	13153_R_AT
1320	13159_AT
1321	13176_AT
1322	13217_S_AT
	17500_S_AT
1323	13225_S_AT
	15997_S_AT
1324	13230_S_AT
	15972_S_AT
1325	13279_S_AT
	17477_S_AT
1326	13280_S_AT
	20301_S_AT
1327	13282_S_AT
	17027_S_AT
1328	13426_AT
1329	13432_AT
1330	13435_AT
1331	13447_S_AT
1332	13474_AT
1333	13511_AT
1334	13546_AT
1335	13547_S_AT
1336	13548_AT
1337	13555_AT
1338	13587_AT
1339	13595_AT
1340	13610_S_AT
1341	13627_AT
1342	13640_AT
1343	13645_AT
1344	13647_AT
1345	13706_S_AT
	19701_S_AT
1346	13716_AT
	18228_AT
1347	13725_AT
1348	13764_AT
1349	13771_AT
1350	13789_AT
1351	13916_AT
1352	13965_S_AT
1353	13967_AT
1354	14028_AT
1355	14039_AT
1356	14046_AT
1357	14049_AT
1358	14069_AT
1359	14077_AT
1360	14080_AT
1361	14083_AT
1362	14089_AT
1363	14090_I_AT
1364	14097_AT
1365	14116_AT
1366	14151_AT
	14219_AT
1367	14170_AT
1368	14172_AT
1369	14192_AT
1370	14224_AT
1371	14227_AT
1372	14244_S_AT
	14245_AT
	14645_S_AT
	15974_G_AT
1373	14248_AT
1374	14250_R_AT
1375	14367_AT
1376	14381_AT
1377	14384_AT
1378	14398_S_AT
1379	14487_AT
1380	14582_AT
1381	14597_AT
1382	14609_AT
1383	14612_AT
	19267_S_AT
1384	14614_AT
1385	14636_S_AT
1386	14644_S_AT
	14658_S_AT
	14659_S_AT
	15964_S_AT
1387	14675_S_AT

TABLE 24 (cont)

1388	14691_AT
	14709_AT
1389	14704_S_AT
	15846_AT
1390	14705_I_AT
1391	14733_S_AT
1392	14735_S_AT
1393	14779_AT
1394	14784_AT
1395	14923_AT
1396	14947_AT
1397	14950_AT
1398	14990_AT
1399	14998_AT
1400	15005_S_AT
1401	15018_AT
1402	15045_AT
1403	15046_S_AT
1404	15052_AT
1405	15058_S_AT
1406	15064_AT
1407	15088_S_AT
1408	15098_S_AT
1409	15103_S_AT
1410	15109_S_AT
1411	15124_S_AT
1412	15127_S_AT
1413	15145_S_AT
1414	15154_S_AT
1415	15161_S_AT
1416	15189_S_AT
1417	15214_S_AT
1418	15255_AT
1419	15356_AT
1420	15357_AT
1421	15364_AT
1422	15392_AT
1423	15403_S_AT
1424	15437_AT
1425	15451_AT
1426	15476_AT
1427	15482_AT
1428	15483_S_AT
1429	15521_S_AT
1430	15522_I_AT
1431	15531_I_AT
1432	15573_AT
1433	15581_S_AT
1434	15586_S_AT
1435	15594_S_AT
1436	15609_S_AT
1437	15611_S_AT
1438	15621_F_AT
1439	15623_F_AT
1440	15669_S_AT
1441	15695_S_AT
1442	15702_S_AT
1443	15753_AT
1444	15761_AT
1445	15776_AT
1446	15778_AT
1447	15839_AT
1448	15842_AT
1449	15857_S_AT
1450	15859_AT
1451	15880_AT
1452	15886_AT
1453	15906_S_AT
1454	15910_AT
1455	15937_AT
1456	15957_AT
1457	15970_S_AT
1458	15985_AT
1459	16010_S_AT
	16011_S_AT
	17078_S_AT
1460	16021_S_AT
1461	16031_AT
1462	16038_S_AT
1463	16045_S_AT
1464	16046_S_AT
1465	16048_AT
1466	16061_S_AT
1467	16082_S_AT
1468	16111_F_AT
1469	16115_S_AT
1470	16141_S_AT
1471	16144_S_AT
1472	16163_S_AT
1473	16173_S_AT
1474	16229_AT
1475	16298_AT
1476	16301_S_AT
1477	16322_AT
1478	16342_AT
1479	16351_AT
1480	16412_S_AT
1481	16422_AT
1482	16427_AT
1483	16438_AT
1484	16474_S_AT
1485	16482_S_AT
1486	16485_S_AT
	18052_S_AT
1487	16493_AT
1488	16534_S_AT
1489	16555_S_AT
1490	16561_S_AT
	17572_S_AT
1491	16592_S_AT
1492	16615_S_AT
1493	16637_S_AT
1494	16692_AT
1495	16712_AT
1496	16789_AT
1497	16818_S_AT
1498	16971_S_AT
1499	17018_S_AT
1500	17019_S_AT
1501	17029_S_AT
1502	17041_S_AT
1503	17047_S_AT
1504	17066_S_AT
1505	17085_S_AT
1506	17089_S_AT
1507	17179_AT
1508	17180_AT
1509	17228_AT
1510	17252_AT
1511	17317_AT
1512	17338_AT
1513	17384_AT
1514	17387_S_AT
1515	17400_S_AT
1516	17407_S_AT
1517	17408_AT
1518	17413_S_AT
1519	17416_AT
1520	17425_S_AT
1521	17440_I_AT
1522	17442_I_AT
1523	17473_AT
1524	17484_AT
1525	17514_S_AT
1526	17520_S_AT
1527	17533_S_AT
1528	17548_S_AT
	19614_AT
1529	17549_S_AT
1530	17555_S_AT
1531	17567_AT
1532	17654_AT
1533	17693_AT
1534	17697_AT
1535	17722_AT
1536	17752_AT
1537	17755_AT
1538	17775_AT
1539	17832_S_AT
1540	17840_S_AT
1541	17843_S_AT
1542	17855_AT
1543	17860_AT
1544	17869_AT
1545	17888_AT
1546	17899_AT
1547	17929_S_AT
1548	17930_S_AT
1549	17932_S_AT
1550	17936_S_AT
	18670_G_AT

TABLE 24 (cont)

1551	17957_AT
1552	17961_AT
1553	17962_AT
1554	17963_AT
1555	17971_S_AT
1556	17975_AT
	18742_F_AT
1557	18016_R_AT
1558	18069_AT
1559	18122_AT
1560	18140_AT
1561	18199_AT
1562	18224_S_AT
1563	18225_AT
1564	18235_AT
1565	18259_S_AT
1566	18265_AT
1567	18270_AT1568
	18280_AT
1569	18289_AT
1570	18296_AT
1571	18298_AT
1572	18314_I_AT
1573	18318_AT
1574	18325_AT
1575	18351_S_AT
1576	18471_AT
1577	18482_S_AT
1578	18484_AT
1579	18560_AT
1580	18564_AT
1581	18590_AT
1582	18594_AT
1583	18595_AT
1584	18596_AT
1585	18629_S_AT
1586	18637_AT
1587	18661_AT
1588	18668_AT
1589	18699_I_AT
1590	18747_F_AT
	18789_AT
1591	18761_AT
1592	18833_AT
1593	18875_S_AT
1594	18894_AT
1595	18936_AT
1596	18946_AT
1597	18953_AT
1598	18955_AT
1599	18972_AT
1600	19008_S_AT
1601	19108_AT
1602	19123_AT
1603	19135_AT
1604	19137_AT
1605	19141_AT
1606	19152_AT
1607	19156_S_AT
1608	19182_AT
1609	19186_S_AT
1610	19214_AT
1611	19216_AT
1612	19227_AT
1613	19243_AT
1614	19288_AT
1615	19359_S_AT
1616	19368_AT
1617	19379_AT
1618	19380_S_AT
1619	19398_AT
1620	19421_AT
1621	19424_AT
1622	19429_AT
1623	19430_AT
1624	19450_AT
1625	19457_AT
1626	19467_AT
1627	19516_AT
1628	19545_AT
1629	19564_AT
1630	19577_AT
1631	19593_AT
1632	19602_AT
1633	19618_AT
1634	19638_AT
1635	19640_AT
1636	19646_S_AT
1637	19656_S_AT
1638	19670_AT
1639	19696_AT
1640	19713_AT
1641	19718_AT
1642	19722_S_AT
1643	19749_AT
1644	19755_AT
1645	19762_AT
1646	19789_S_AT
1647	19815_AT
1648	19843_AT
1649	19869_AT
1650	19878_AT
1651	19883_AT
1652	19894_AT
1653	19926_AT
1654	19944_AT
1655	19968_AT
1656	19977_AT
1657	19982_AT
1658	19987_AT
1659	19991_AT
1660	20015_AT
1661	20017_AT
1662	20031_AT
1663	20040_AT
1664	20042_S_AT
1665	20060_AT
	20438_AT
1666	20089_AT
1667	20118_AT
1668	20144_AT
1669	20149_AT
1670	20179_AT
1671	20190_AT
1672	20194_AT
1673	20219_AT
1674	20245_S_AT
1675	20263_AT
1676	20308_S_AT
1677	20335_S_AT
1678	20338_AT
1679	20345_AT
1680	20365_S_AT
1681	20382_S_AT
1682	20390_S_AT
1683	20395_AT
1684	20420_AT
1685	20421_AT
1686	20432_AT
1687	20437_AT
1688	20442_I_AT
1689	20463_S_AT
1690	20491_AT
1691	20537_AT
1692	20573_AT
1693	20636_AT
1694	20638_AT
1695	20641_AT
1696	20658_S_AT
1697	20689_S_AT
1698	20698_S_AT

TABLE 25: 2X UP IN COLD, SALT & MANNITOL

12023_s_at	14733_s_at	17047_s_at	19640_at
12332_s_at	14923_at	17179_at	19646_s_at
12530_at	14990_at	17180_at	19656_s_at
12536_s_at	15005_s_at	17252_at	19701_s_at
12574_at	15018_at	17384_at	19843_at
12595_at	15052_at	17407_s_at	19944_at
12698_at	15088_s_at	17484_at	19982_at
12749_at	15098_s_at	17520_s_at	19987_at
12765_at	15103_s_at	17555_s_at	19991_at
12769_at	15145_s_at	17572_s_at	20042_s_at
12785_at	15154_s_at	17722_at	20060_at
12857_at	15161_s_at	17752_at	20118_at
12964_at	15214_s_at	17840_s_at	20144_at
12972_at	15356_at	17843_s_at	20149_at
12989_s_at	15521_s_at	17860_at	20179_at
13004_at	15573_at	17929_s_at	20194_at
13025_at	15586_s_at	17936_s_at	20245_s_at
13036_at	15609_s_at	17962_at	20390_s_at
13099_s_at	15611_s_at	18052_s_at	20437_at
13136_at	15621_f_at	18069_at	20463_s_at
13176_at	15669_s_at	18122_at	20491_at
13220_s_at	15695_s_at	18199_at	20641_at
13225_s_at	15753_at	18259_s_at	20658_s_at
13230_s_at	15761_at	18280_at	
13239_s_at	15857_s_at	18289_at	
13426_at	15871_s_at	18314_i_at	
13474_at	15964_s_at	18318_at	
13548_at	15970_s_at	18325_at	
13555_at	15974_g_at	18482_s_at	
13595_at	15997_s_at	18590_at	
13627_at	16011_s_at	18594_at	
13645_at	16021_s_at	18595_at	
13647_at	16038_s_at	18596_at	
13706_s_at	16046_s_at	18629_s_at	
13965_s_at	16082_s_at	18661_at	
13967_at	16111_f_at	18668_at	
14080_at	16115_s_at	18699_i_at	
14090_i_at	16127_s_at	18722_s_at	
14097_at	16141_s_at	18936_at	
14116_at	16144_s_at	18953_at	
14151_at	16163_s_at	18955_at	
14172_at	16236_g_at	18972_at	
14192_at	16301_s_at	19008_s_at	
14244_s_at	16322_at	19152_at	
14245_at	16422_at	19186_s_at	
14367_at	16474_s_at	19214_at	
14398_s_at	16482_s_at	19368_at	
14582_at	16485_s_at	19379_at	
14614_at	16555_s_at	19380_s_at	
14644_s_at	16561_s_at	19421_at	
14645_s_at	16592_s_at	19545_at	
14658_s_at	16637_s_at	19614_at	
14659_s_at	17041_s_at	19638_at	

TABLE 26: 2X DOWN IN COLD, MANNITOL & SALT, ONLY

12078_at	15189_s_at	17869_at	20015_at
12115_at	15357_at	17888_at	20040_at
12118_at	15364_at	17930_s_at	20089_at
12150_at	15403_s_at	17932_s_at	20190_at
12271_s_at	15476_at	17957_at	20219_at
12276_at	15483_s_at	17963_at	20263_at
12338_at	15522_i_at	17971_s_at	20301_s_at
12400_at	15531_i_at	17975_at	20308_s_at
12430_at	15594_s_at	18016_r_at	20338_at
12538_at	15702_s_at	18140_at	20345_at
12622_at	15778_at	18224_s_at	20395_at
12630_at	15839_at	18225_at	20442_i_at
12792_s_at	15842_at	18228_at	20537_at
12805_s_at	15859_at	18235_at	20573_at
12883_s_at	15872_at	18265_at	20636_at
12909_s_at	15880_at	18270_at	20638_at
12932_s_at	15886_at	18296_at	20698_s_at
12968_at	15906_s_at	18298_at	
13159_at	15957_at	18471_at	
13217_s_at	15985_at	18564_at	
13279_s_at	16045_s_at	18637_at	
13282_s_at	16061_s_at	18742_f_at	
13432_at	16173_s_at	18761_at	
13511_at	16298_at	18833_at	
13546_at	16351_at	18875_s_at	
13547_s_at	16412_s_at	18894_at	
13587_at	16438_at	18946_at	
13610_s_at	16493_at	19123_at	
13640_at	16534_s_at	19216_at	
13725_at	16539_s_at	19243_at	
13771_at	16615_s_at	19267_s_at	
13916_at	16692_at	19288_at	
14028_at	16789_at	19398_at	
14039_at	16818_s_at	19424_at	
14046_at	16971_s_at	19430_at	
14049_at	17018_s_at	19450_at	
14077_at	17029_s_at	19457_at	
14170_at	17089_s_at	19467_at	
14227_at	17228_at	19516_at	
14248_at	17338_at	19564_at	
14381_at	17387_s_at	19577_at	
14384_at	17413_s_at	19593_at	
14487_at	17416_at	19602_at	
14597_at	17425_s_at	19618_at	
14705_i_at	17440_i_at	19670_at	
14709_at	17473_at	19696_at	
14779_at	17533_s_at	19722_s_at	
14947_at	17549_s_at	19749_at	
14950_at	17654_at	19755_at	
14998_at	17693_at	19815_at	
15045_at	17697_at	19926_at	
15109_s_at	17755_at	19968_at	
15124_s_at	17832_s_at	19977_at	

TABLE 27: 2X ROOT SPECIFIC (COLD, SALINE & OSMOTIC STRESSES)

11997_at	14069_at	16052_at	18327_s_at
12004_at	14072_at	16053_i_at	18597_at
12051_at	14073_at	16105_s_at	18607_s_at
12072_at	14097_at	16161_s_at	18636_at
12150_at	14139_at	16165_s_at	18663_s_at
12151_at	14235_at	16298_at	18782_at
12166_i_at	14250_r_at	16334_s_at	18885_at
12219_at	14578_s_at	16422_at	18888_at
12315_at	14582_at	16427_at	18942_at
12332_s_at	14640_s_at	16440_s_at	18955_at
12374_i_at	14643_s_at	16442_s_at	19060_at
12482_s_at	14644_s_at	16468_at	19108_at
12515_at	14658_s_at	16488_at	19135_at
12522_at	14659_s_at	16511_at	19137_at
12538_at	14711_s_at	16529_at	19195_at
12571_s_at	14900_at	16553_f_at	19263_at
12574_at	14924_at	16568_s_at	19376_at
12609_at	14990_at	16914_s_at	19406_at
12678_i_at	15018_at	16965_s_at	19432_s_at
12698_at	15022_at	16981_s_at	19835_at
12749_at	15107_s_at	16989_at	19836_at
12760_g_at	15116_f_at	17033_s_at	19840_s_at
12765_at	15120_s_at	17066_s_at	19841_at
12768_at	15124_s_at	17085_s_at	19843_at
12769_at	15131_s_at	17252_at	19926_at
12772_at	15132_s_at	17376_at	19972_at
12777_i_at	15137_s_at	17378_at	19977_at
12958_at	15184_s_at	17388_at	19991_at
12989_s_at	15188_s_at	17415_at	20034_i_at
13015_s_at	15208_s_at	17429_s_at	20042_s_at
13134_s_at	15252_g_at	17463_at	20189_at
13146_s_at	15343_at	17485_s_at	20194_at
13172_s_at	15389_at	17490_s_at	20200_at
13178_at	15392_at	17567_at	20214_i_at
13179_at	15448_at	17585_s_at	20239_g_at
13187_i_at	15503_at	17595_s_at	20262_at
13211_s_at	15531_i_at	17840_s_at	20269_at
13239_s_at	15594_s_at	17860_at	20294_at
13273_s_at	15609_s_at	17880_s_at	20312_s_at
13297_s_at	15623_f_at	17894_at	20382_s_at
13549_at	15639_s_at	17896_at	20396_at
13604_at	15670_s_at	17899_at	20432_at
13629_s_at	15680_s_at	17911_at	20444_at
13706_s_at	15859_at	17935_at	20446_s_at
13714_at	15900_at	17961_at	20480_s_at
13751_at	15923_at	18024_s_at	20586_i_at
13895_at	15962_s_at	18122_at	20612_s_at
13933_at	15964_s_at	18222_at	20672_at
13967_at	15965_at	18224_s_at	20686_at
13985_s_at	15975_s_at	18252_at	20689_s_at
14028_at	15985_at	18255_at	
14030_at	16001_at	18269_s_at	
14058_at	16048_at	18270_at	

TABLE 28: 2X LEAF SPECIFIC (COLD, SALINE & OSMOTIC STRESSES)

12169_i_at	16136_s_at
12186_at	16172_s_at
12187_at	16316_at
12211_at	16385_s_at
12212_at	16455_at
12214_g_at	16485_s_at
12270_at	16512_s_at
12645_at	16547_s_at
12754_g_at	16548_s_at
12774_at	16629_s_at
12793_at	16673_at
12796_s_at	16899_at
12910_s_at	17010_s_at
12916_s_at	17018_s_at
12953_at	17054_s_at
13090_at	17095_s_at
13124_at	17097_s_at
13335_at	17273_at
13550_at	17394_s_at
13567_at	17420_at
13568_at	17449_s_at
13596_at	17600_s_at
13614_at	17843_s_at
13678_s_at	17913_s_at
13719_at	17966_at
14014_at	18003_at
14096_at	18081_at
14118_i_at	18560_at
14369_at	18588_at
14478_at	18626_at
14513_s_at	18644_at
14540_at	18666_s_at
14596_at	18742_f_at
14733_s_at	18977_at
14986_at	18994_at
15045_at	19227_at
15097_s_at	19373_at
15098_s_at	19834_at
15145_s_at	19867_at
15153_s_at	19998_at
15154_s_at	20062_at
15182_s_at	20199_at
15203_s_at	20256_s_at
15372_at	20284_at
15521_s_at	20437_at
15581_s_at	20442_i_at
15621_f_at	20450_at
15642_s_at	20468_at
15776_at	20547_at
15910_at	20635_s_at
16017_at	
16046_s_at	
16115_s_at	

TABLE 29: 2X TRANSCRIPTION (COLD, SALINE & OSMOTIC STRESSES)

12068_at	15665_s_at	19836_at
12166_i_at	15679_s_at	19860_at
12374_i_at	15720_at	19866_at
12392_at	15871_s_at	19898_at
12431_at	16072_s_at	20262_at
12450_s_at	16073_f_at	20335_s_at
12503_at	16105_s_at	20362_at
12536_s_at	16111_f_at	20424_at
12540_s_at	16127_s_at	20437_at
12541_at	16534_s_at	20456_at
12587_at	16582_s_at	20515_s_at
12594_at	16589_s_at	20635_s_at
12595_at	16747_at	
12704_f_at	17019_s_at	
12705_f_at	17129_s_at	
12709_f_at	17160_at	
12712_f_at	17520_s_at	
12719_f_at	17538_s_at	
12724_f_at	17555_s_at	
12725_r_at	17609_at	
12726_f_at	17896_at	
12734_f_at	17971_s_at	
12736_f_at	17975_at	
12737_f_at	17978_s_at	
12812_at	18121_s_at	
12949_at	18167_s_at	
12951_at	18197_at	
12966_s_at	18222_at	
13023_at	18318_at	
13034_s_at	18576_s_at	
13087_at	18629_s_at	
13270_at	18738_f_at	
13273_s_at	18742_f_at	
13432_at	18744_f_at	
13555_at	18745_f_at	
13688_s_at	18747_f_at	
13714_at	18750_f_at	
13965_s_at	18751_f_at	
13987_s_at	18789_at	
14003_at	18834_at	
14144_at	18942_at	
14178_at	19083_at	
14223_at	19202_at	
14235_at	19209_s_at	
14303_s_at	19232_s_at	
14393_at	19315_at	
14553_at	19489_s_at	
14781_at	19611_s_at	
15046_s_at	19646_s_at	
15053_s_at	19707_s_at	
15214_s_at	19722_s_at	
15510_r_at	19744_at	
15638_s_at	19755_at	

TABLE 30: 2X PHOSPHATES (COLD, SALINE & OSMOTIC STRESSES)

12470_at
12556_at
13128_at
13135_s_at
13180_s_at
13192_s_at
13193_s_at
13587_at
13995_at
14335_at
15073_at
15171_s_at
15240_at
15586_s_at
15641_s_at
15651_f_at
15990_at
16232_s_at
16576_f_at
16753_at
17423_s_at
17525_s_at
17537_s_at
17929_s_at
17954_s_at
18012_s_at
18308_i_at
18616_at
18847_at
18936_at
18980_at
19243_at
19263_at
19638_at
19883_at
19932_at
20333_at
20393_at
20570_at

TABLE 31: 2X KINASES (COLD, SALINE & OSMOTIC STRESSES)

12253_g_at	16059_s_at	20144_at
12270_at	16087_s_at	20219_at
12271_s_at	16088_f_at	20223_at
12276_at	16125_s_at	20232_s_at
12278_at	16137_s_at	20235_i_at
12284_at	16140_s_at	20282_s_at
12300_at	16143_s_at	20298_at
12307_at	16144_s_at	20396_at
12353_at	16160_f_at	20439_at
12357_s_at	16171_s_at	20462_at
12390_at	16357_at	
12394_at	16412_s_at	
12395_s_at	16568_s_at	
12408_at	16570_s_at	
12452_at	16571_s_at	
12477_at	16584_s_at	
12490_at	16651_s_at	
12497_at	16652_s_at	
12532_at	16672_at	
12697_at	16818_s_at	
12901_s_at	16840_at	
12902_at	17068_s_at	
12958_at	17122_s_at	
12959_at	17252_at	
13068_at	17323_at	
13246_at	17475_at	
13324_at	17752_at	
13332_at	17921_s_at	
13362_s_at	17933_at	
13370_at	17935_at	
13550_at	18013_r_at	
14030_at	18046_s_at	
14048_at	18122_at	
14194_at	18176_at	
14196_at	18316_at	
14217_at	18455_at	
14459_at	18459_at	
14603_at	18482_s_at	
14637_s_at	18543_at	
14686_s_at	18706_s_at	
15005_s_at	18782_at	
15175_s_at	18924_at	
15270_at	19117_s_at	
15475_s_at	19437_s_at	
15497_s_at	19442_at	
15577_s_at	19458_at	
15616_s_at	19464_at	
15633_s_at	19469_at	
15634_s_at	19562_at	
15668_s_at	19655_at	
15680_s_at	19749_at	
15798_at	19854_at	
16034_at	19904_at	